

2964

PTO-1542
(4-85)

RECEIVED
STIC

U.S. DEPARTMENT OF COMMERCE
PATENT AND TRADEMARK OFFICE

ONLINE SEARCH REQUEST FORM

USER SPECTOR

SEP 22 1995
SERIAL NUMBER 386680

ART UNIT 1812

PHONE 308-1793

DATE 9/22/95

Please give a detailed statement of requirements. Describe as specifically as possible the subject matter to be searched. Define any terms that may have special meaning. Give examples or relevant citations, authors, or keywords, if known.

You may include a copy of the broadest and or relevant claim(s).

Please search commercial & interference
& issued databases for
Seq ID No: 1 of 08/167628 (parent)

If possible, do search of EST's & STS's
separately (not lumped in with everything
else) - ~~if this~~ it obscures results if all done
at once
Thanks

4/20/95 C RFA seq moved
to public database

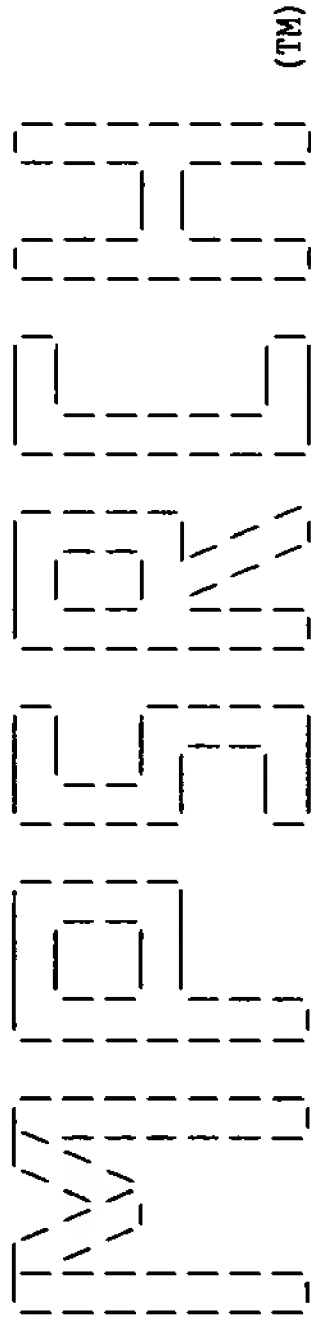
PN = 5,408,040

STAFF USE ONLY

COMPLETED 9-24-95
SEARCHER JILIP X 308 4268
ONLINE TIME 16 TOTAL TIME 20
(in minutes)
NO. OF DATABASES 2

SYSTEMS

☐ CAS ONLINE
☐ DARC/QUESTEL
☐ DIALOG
☒ SDC
☐ OTHER mp srua



Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Sep 22 22:17:35 1995; MasPar time 117.89 Seconds
898.163 Million cell updates/sec

Tabular output not generated.

Title: >US-08-167-628-1
Description: (1:2075) from 5408040.seq
Perfect Score: 2075
N.A. Sequence: 1 CCCGGCCGACAGCCCGGAGAG.....AGGAAATGTGGTAGCTCAGC 2075
Comp: GGGCGGCTGTCTCGGGGTCT.....TCCTTTACACCATCGAGTGC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 61539 seqs, 25515148 bases x 2

Database: n-genseq
1 n-gen1
2 n-gen2
3 n-gen3
4 n-gen4
5 n-gen5
6 n-gen6
7 n-gen7
8 n-gen8
9 n-gen9
10 n-gen10
11 n-gen11

Statistics: Mean 10.059; Variance 7.188; scale 1.400

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	921	44.4	2330	4	Gene for beta-IG-M2.	0.00e+00
2	264	12.7	1975	6	Chicken nov coding se	2.19e-132
3	240	11.6	619	6	Human sequence XXVII	2.44e-118
4	215	10.4	684	6	Chicken nov gene frag	9.12e-104

5	160	7.7	461	6	Q36044	Chicken nov gene exon	5.23e-72
6	106	5.1	252	6	Q36035	Chicken nov gene exon	1.64e-41
7	106	5.1	196	6	Q36045	Chicken nov gene exon	1.64e-41
8	103	5.0	131	6	Q36049	Fragment XXXII encode	7.54e-40
9	88	4.2	2028	4	Q26421	Gene for beta-IG-M1.	1.28e-31
10	80	3.9	1047	2	Q10572	Human Natriuretic Pep	2.72e-27
11	79	3.8	1047	2	Q10572	Human Natriuretic Pep	9.36e-27
12	67	3.2	372	10	Q57417	CYR61 like protein.	2.18e-20
13	65	3.1	216	6	Q36039	Homologous to exon 3	2.43e-19
14	65	3.1	435	6	Q36040	Homologous to exon 4	2.43e-19
15	65	3.1	216	6	Q36041	Homologous to chicken	2.43e-19
16	64	3.1	230	6	Q36033	Chicken nov gene exon	8.05e-19
17	63	3.0	209	6	Q36038	Chicken nov gene exon	2.66e-18
18	62	3.0	452	6	Q36037	Sequence XI homologou	8.78e-18
19	62	3.0	253	6	Q36036	Encodes polypeptide h	8.78e-18
20	60	2.9	72	6	Q36047	Human sequence XXVIII	9.45e-17
21	54	2.6	142	6	Q36048	Chicken nov gene 4th	1.08e-13
22	52	2.5	632	6	Q36034	Chicken nov gene frag	1.09e-12
23	44	2.1	204	1	N81164	Base substituted E.co	9.28e-09
24	44	2.1	91	9	Q51746	Oligonucleotide probe	9.28e-09
25	43	2.1	91	9	Q51746	Oligonucleotide probe	2.80e-08
26	43	2.1	204	1	N81164	Base substituted E.co	2.80e-08
27	39	1.9	56	5	Q33947	Microsatellite sequen	2.17e-06
28	38	1.8	60	5	Q33792	Microsatellite sequen	6.31e-06
29	36	1.7	63	5	Q33701	Microsatellite sequen	5.20e-05
30	35	1.7	1521	5	Q29724	Sequence of the first	1.47e-04
31	34	1.6	258	5	Q32866	Probe VAW409 for diag	4.12e-04
32	34	1.6	40	4	Q34094	Sequence of a microsa	4.12e-04
33	34	1.6	53	5	Q33627	Microsatellite sequen	4.12e-04
34	33	1.6	3871	2	N71302	HSV-1 gB and surround	1.14e-03
35	33	1.6	266	4	Q27097	Fragile X diagnostic	1.14e-03
36	33	1.6	840	4	Q29612	Encodes carp TLIIbet	1.14e-03
37	33	1.6	49	4	Q34122	Sequence of a microsa	1.14e-03
38	33	1.6	59	4	Q34173	Sequence of a microsa	1.14e-03
39	32	1.5	327	10	Q77289	Human genome fragment	3.13e-03
40	32	1.5	50	4	Q34167	Sequence of a microsa	3.13e-03
41	32	1.5	870	6	Q39248	Sequence of cosmid cl	3.13e-03
42	32	1.5	62	4	Q34053	Microsatellite sequen	3.13e-03
43	31	1.5	79	4	Q33502	Sequence of microsa	8.49e-03
44	31	1.5	260	10	Q77444	Human genome fragment	8.49e-03
45	30	1.4	201	2	N70195	Streptomyces protease	2.27e-02

ALIGNMENTS

RESULT	1
ID	Q26422 standard; DNA; 2330 BP.
AC	Q26422;
DT	18-JAN-1993 (first entry)
DE	Gene for beta-IG-M2.
KW	Transforming growth factor beta; induced; CEF-10; v-src; chicken;
KW	embryo; fibroblasts; TGF-beta; ss.
OS	Mus musculus.
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	/*tag= a
PN	EP-495674-A.
PD	22-JUL-1992.
PF	17-JAN-1992; 300429.
PR	18-JAN-1991; US-642991.
PR	10-JAN-1992; US-816270.
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
PI	Brunner AM, Chinn J, Neubauer MG, Purchio AF;
DR	WPI; 92-243508/30.

DR P-PSDB; R25565.
PT TGF-beta induced gene family - encodes proteins involved in
PT growth and differentiation effects of TGF-beta-1
PS Claim 7; Fig 2; 35pp; English.
CC The DNA encoding mouse beta-IG-M2 was obtd. from AKR-2B mouse cells
CC induced with TGF-betal and cyclohexamide. Poly RNA extracted from
CC these cells was used to create a cDNA library which was screened
CC using two probes. The probes were prepd. from untreated AKR-2B mRNA
CC and AKR-2B mRNA from cells treated with cyclohexamide and TGF-betal.
CC Hybridising colonies were isolated and two clones (beta-IG-M1 and
CC beta-IG-M2) were then sequenced. The DNA encodes proteins that
CC have a 80 and 50 percent homology respectively with the CEF-10
CC protein induced by v-src in chicken embryo fibroblasts. The
CC proteins encoded by TGF-beta induced genes are likely to be
CC involved in mediation of the biological effects of TGF-beta
CC relating to cell growth and differentiation.
CC See also Q26421.
SQ Sequence 2330 BP; 589 A; 598 C; 595 G; 548 T;

DB 4; Score 921; Match 80.8%; QryMatch 44.4%; Pred. No. 0.00e+00;
Matches 1544; Conservative 0; Mismatches 317; Indels 51; Gaps 29;

Db 241 tsgtgcctctgcacctctgcaccggcctgtctacgggccagactgaagcgccaatgtc 300
||||| ||||||| ||||||| || ||||| ||||||| || |||
Qy 170 TGTCTCTCTCGCCCTCTGCAGCGCGCGCGCTGCGGCCAGAACTGCAGCGGGCGGTGCC 229

Db 301 agtgcgagccgaagcagcgccgcactgccccgcggcgtagcctggctgtgagcggt 360
||||| | ||| | ||||||| ||||||| || ||||||| || ||||||| |||||
Qy 230 GGTGCCCGGAGAGCGCGCGCGCTGCCGGCGGCGGTGAGCCTCGTGTGGACGGCT 289

Db 361 gcggtgctgcgcgtctgcgccagcagctgggagaactgtgtacggagcgtgacct 420
||||||||| ||||||| ||||||| || ||||| || ||||| || ||||| |||||
Qy 290 GCGGCTGTCGCGGTCTGCGCCAGCAGCTGGGCGAGCTGTGCACCGCGCACCCCT 349

Db 421 gsgaccacacaagggcctcttctgcgatttcggctcccccgcccaaccgaagattggag 480
||||||| ||||||| ||||||| || ||||||| || ||||||| || ||||||| |||
Qy 350 GCGACCGCACAAAGGGCCTCTTCTGTGACTTCGGCTCCCGGCCAACCGCAAGATCGGCG 409

Db 481 tgtgcactgccaaagatggtgcacctgtgtcttcgtggctcggtgacctgagcggtg 540
||||||| ||||||| ||||||| ||||| ||||||| || ||||||| || ||||||| |||||
Qy 410 TGTGCACGCCAAAGATGTTGCTCCCTGCACTTTCGTTGGTGTACGGTGTACCGAGCGGAG 469

Db 541 agtccttccaaagcagctgcaaaataccaatgcacttgccctggatgggcccgtggctcgg 600
||||||| ||||||| ||||||| ||||| ||||| ||||||| ||||| ||||||| |||||
Qy 470 AGTCCTTCCAGAGCAGCTGCAAGTACCAGTGCACGTGCCTGCACGGCGGTGGGCTGCA 529

Db 601 tgccccctatgcagcatggacgtgcgcctgccccagccctgactgccccttcccagagaagg 660
||||||| ||||||| ||||||| || ||||||| ||||||| ||||||| ||||||| |||||
Qy 530 TGCCCTCTGCAGCATGGACGTTCCGTCTGCCAGCCCTGACTGCCCTTCCCGAGGAGGG 589

Db 661 tcaagctgcctgggaaaatgctgcgaggagtggggtgtgtgaacgagcccaaggaccgcacag 720
||||||| || ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Qy 590 TCAAGCTCCCGGAAATGCTGCGAGGAGTGGGTGTGTGACGAGCCCAAGGACCAACCG 649

Db 721 cagttgcccctgcccctagctgcctaccgactggaagacacatttggcccagaccacaacta 780
||||| ||||||| || || ||||||| ||||||| || ||||||| ||||||| |||||
Qy 650 TGGTTGGCCTGCGCTCGCGGCTTACCGACTGGAAACACACGTTTGGCCAGACCCAACTA 709

Db 781 tgatgcagccaaactgcctgggtccagaccacagatggagcgccctgttcttaagacctgtg 840
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Qy 710 TGATTAGACCCAACTGCCCTGGTCCAGACCAGAGTGGAGCGCCTGTTCAAACACCTGTG 769

Db 841 gaatgggcatctccaccggatttaccaatgacaataaccttctgcagactggagaagcaga 900
| ||||||| ||||||| ||||||| ||||| || ||||| || ||||||| |||||

Qy 770 GGATGGGCATCTCCACCCGGGTTACCAATGCAACCGCCTCCTGCAGGCTAGAGAAGCAGA 829

Db 901 gccgcctctgcatggtcaggccctcggaagctgacctggaggaaaaacattaaagaaggca 960
||||||| ||||||| ||||||| ||||||| ||||||| ||||| || ||||||| |||||
Qy 830 GCCGCCTGTGCATGGCTCAGGCCCTTGCGAAGCTGACCTGGAAAGACAATTAAGAAGGGCA 889

Db 961 aaaagtgcatccggacacacctaaatcgccaagcctgtcaagtttgagctttctggctgca 1020
||||| ||||||| || || ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Qy 890 AAAAGTGCATCCGTACTCCCAAAATCTCCAAGCCTATCAAGCTTTTGAGCTTTCTGGCTGCA 949

Db 1021 ccagtgtgaagacatacaggggctaagttctcggggtgtgtgeacagacggccgctgctgca 1080
||||| ||||||| || ||||| ||||| ||||| ||||| || || ||||| |||||
Qy 950 CCAGCATGAAGACATACCAGAGCTAAATTTCTGTGGAGTATGTACCCGACGGCCGATGCTGCA 1009

Db 1081 caccgcacagaaccaccactctgccagtgaggttcaaatgccccgatggcgagatcatga 1140
|| || ||||||| ||||| ||||| ||||||| ||||| ||||| || ||||| |||||
Qy 1010 CCCCCACAGAACCACCACCTGCCGGTGGAGTTCAAGTGCCTTGACGGCGAGGTCATGA 1069

Db 1141 aaaagaatatgatgttcatacaagaccctgtgcctgceattacaactgtcctggggacaatg 1200
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| || |||||
Qy 1070 AGAAGAACATGATGTTCAATCAAGACCTGTGCTGCCAATTACAACCTGTCCCGAGACAAATG 1129

Db 1201 acatctttgagtccectgtactacaggaagatgtacggagacatggcgtaagccagggaag 1260
||||| ||||| || ||||||| ||||||| ||||||| ||||||| || ||||| ||
Qy 1130 ACATCTTTGAATCGCTGTACTACAGGAAGATGTACGAGACATGGCATGAAGCCAGAGAG 1189

Db 1261 taagggaacgaactcattagactataaactgaactgagttgcatactcattttctctgt 1320
|| || ||||| ||||||| ||||| ||||||| || ||||||| || ||||||| || |||
Qy 1190 TGAGAGACATTAACCTCATTAGACTGGAACCTTGAACCTGATTCAATCTCATCTCATTTT--TCCGT 1247

Db 1321 aaaaaaattacagtagecat--taatttaaactctgtgttttaactaccgtgggagga 1379
||||| ||||| ||||||| || ||||||| || ||||||| || ||||| || |||||
Qy 1248 AAAAAATGATTTCACTAGCACAAAGTTATTTAAATCTGTTTCTTAACTG--G-GGGAANAAG 1304

Db 1380 ctatccccaccaaaagtgagaacgtttatgtcatggccatacaaatgtctgtcaacctcaga 1439
| ||||||| || | ||||| || ||||| || ||||| || ||||| || |||||
Qy 1305 AT-TCCCACCCCAATTCAAAAACATTTGTGCCATGTCAA-ACAAATAGTCTATCTTCCCCCAGA 1362

Db 1440 cactggtttcgagacagtttacacttgacagtgtg--t-cattagcgcacagtgccagaa 1496
||||||| ||||| ||||| ||||||| || ||||||| || ||||||| |||||
Qy 1363 CACTGGTTTGAAGAATGTTAAGACTTGACACTGGAACACTACATTAGTACACAGCACCCAGAA 1422

Db 1497 cgcacactgagtgagtcctcctggaaacagtgagatgccaggagaaagaaagacaggtac 1556
| | | ||||| | || ||||| || ||||| || | | | | | || |||||
Qy 1423 TGTATATTAAAGGTGTGGCTTTAGGAGCAGTGG-GAGGGTACCGGCCCG---GTTAG-TAT 1477

Db 1557 tagctgaggttattttaaaagcagcagtgctgcctacttttggagtgtaacccggggaggg 1616
| | | | | ||||| ||||| || ||||| || ||||| || ||||| || |||||
Qy 1478 CATCAGATCGACTCTTATACG-AGTAATATGCCTGCTATTTTGAAGTGTAAATTGAGAAGGA 1536

Db 1617 aaattatagcatgcttgcagacagacctg---ctctagcagagctgagca-tgtgtcct 1672
||||| ||||| ||||| || ||||| | ||||| || ||||| || ||||| || |||||
Qy 1537 AAATTTTAGCGTGTCACTGACCTGCTGTACCCCGAGTGACAGCTAGGATGTGCATTCT 1596

Db 1673 cca-ctag-atgaggctgagtcagactgttctttaag-----aacagacttcaagctctg 1726
||| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1597 CCAGCCATCAAGAGACTGACTCAAGTTGTTCTCTTAAGTCAGAAACAGAGACTCAGCTCTG 1656

Db 1727 accattctgattccagtgacacttgtcaggagtcagagccttgtctgttagactggacag 1786
|| ||||||| || ||||||| ||||| || ||||| || ||||| ||||| |||||
Qy 1657 AC-ATTCTGATTCCAATGACACTGTTTCAAGAAATCGGAATCCTGTTCGATTAGACTGGACAG 1715

Db 1787 cttgtggcaagtaagtttgcctgtacaagaccagacttttt-----attgatattgtaaata 1842
||||||| ||||| | ||||||| ||||||| ||||| ||||| ||||| |||||

Db	506	ttgaacagacaagaatgagtgcttgttccaaaagctgtggaatgggctttttaccc	565
Qy	728	TGGTCCAGACCAAGAGTGGAGCGGCTGTTCCAAAGACCTGTGGGATGGGCATCTCCACCC	787
Db	566	gtgttaccacaagaatacagcagtgatgagatgggtgaagcagacacgactttgcatgatga	625
Qy	788	GGGTTACCAAATGACAACGGCTCCTGCAGGCTAGAGAAGCAGAGCCGCCCTGTGCAATGGTCA	847
Db	626	gaccttgtgaa	636
Qy	848	GGCCTTGCGAA	858

RESULT	5	
ID	Q36044	standard; cDNA; 461 BP.
AC	Q36044;	
DT	24-MAY-1993	(first entry)
DE	Chicken nov gene exon 3-4	fragment XXII.
KW	avian nephroblastoma;	avian myeloblastoma virus;
KW	stringent hybridisation;	ss.
OS	Gallus domesticus.	
PN	W09300430-A.	
PD	07-JAN-1993.	
PF	25-JUN-1992;	F00589.
PR	25-JUN-1991;	FR-007807.
PA	(CNRS) CENT NAT RECH SCI.	
PI	Martinerie C, Perbal B;	
DR	WPI; 93-036377/04.	
PT	Nucleotide sequences	hybridising to regions of chicken nov gene -
PT	useful as probes for	detecting complementary sequences to
PT	evaluate development	and/or differentiation of tumours
PS	Claim 20; Page 38;	67pp; French.
CC	The chicken nov gene	is stimulated in avian nephroblastoma induced
CC	by avian myeloblastoma	virus but not in normal adult kidney. A
CC	1975bp cDNA sequence	(Q36031) was isolated from a gene bank prepared
CC	from chicken embryonic	fibroblasts screened with a tumour-derived
CC	probe. Fragment XXII	is part of the 3rd and 4th exons of the nov gene;
CC	nucleotide sequences	which hybridise to Fragment XXII under stringent
CC	conditions (i.e. 50%	formamide, 5 x SCC) are claimed. The claimed
CC	sequences preferably	encode a protein with the sequence XXIII
CC	(R31608) or encode a	protein with at least 60% homology to it.
SQ	Sequence 461 BP;	109 A; 116 C; 143 G; 93 T;

DB	6;	Score	160;	Match	68.9%;	QryMatch	7.7%;	Pred. No.	5.23e-72;
Matches	292;	Conservative	0;	Mismatches	132;	Indels	0;	Gaps	0;

Db	17	ctgcgttctcgatgggatgattaccgcgaacggggaacagcttcacgccagctgcaagta	76
Qy	435	CTGCATCTTCGGTGGTACGGTGTACGCAGCGGAGAGTCCCTTCAGAGCAGCTGCAAGTA	494
Db	77	ccagtgaacctgcgcgggaacgggcagatcggtgcctgccccggtgcaacctgggcctgct	136
Qy	495	CCAGTGCACGTCCTGGACGGGGCGGTGGCTGCATGCCCTCTGCAGCATGGACGCTTCG	554
Db	137	gtccccggccccgactgcacctcccgcggaagatcgaaagtcctcccgagagtgctgcga	196
Qy	555	TCGCCACGCCCCTACTGCCCTTCGCCGAGGAGGGTCAAGCTGCCCGGGAATGCTGCCGA	614
Db	197	gaagtgggtgtgcgaccccaaggatgaagtgtcctcctgggaggtttgtctatggctgcata	256
Qy	615	GGAGTGGGTGTCTACGAGGCCCAAGACCCTGGTTGGCGCTGCCCTCGCGGCTTA	674
Db	257	cagacaggagggccacacttgggatagacgtgtctgattcaagtgcccaattgtattgaaca	316

Qy	675	CGACTGGAAGACACAGT	TTGGCCAGACCCAACTATGATTAGAGCCAACTGCCTGGTCCA	734
Db	317	gacaacagaatgagtgctt	gttccaaaaagctgtggaatgggctttttctaccogtgttac	376
Qy	735	GACCACAGTGGAGCGCCT	GTTCGAAGACCTGTGGGATGGGCATCTCCACCCGGGTTAC	794
Db	377	caacagaatcagcagtg	gagatggtgaagcagacacgactttgcatgatgagaccttg	436
Qy	795	CAATGACACGGCTCCT	TGCGAGGCTAGAGAACGACAGCGCGCTGTGCATGGTCAGGCCCTTG	854
Db	437	tga	440	
Qy	855	CGAA	858	

RESULT 6

ID Q36035 standard; cDNA; 252 BP.
AC Q36035;
DT 24-MAY-1993 (first entry)
DE Chicken nov gene exon 3 fragment VIII.
KW avian nephroblastoma; avian myeloblastoma virus;
KW stringent hybridisation; ss.
OS Gallus domesticus.
PN M09300430-A.
PD 07-JAN-1993.
PF 25-JUN-1992; F00589.
PR 25-JUN-1991; FR-007807.
PA (CNRS) CENT NAT RECH SCI.
PI Martinerie C. Perbal B;
DR WPI; 93-036377/04.
DR P-PSDB; R31602.
PT Nucleotide sequences hybridising to regions of chicken nov gene -
PT useful as probes for detecting complementary sequences to
PT evaluate development and/or differentiation of tumours
PS Claim 7; Page 30; 67pp; French.
CC The chicken nov gene is stimulated in avian nephroblastoma induced
CC by avian myeloblastoma virus but not in normal adult kidney. A
CC 1975bp cDNA sequence (Q36031) was isolated from a gene bank prepared
CC from chicken embryonic fibroblasts screened with a tumour-derived
CC probe. Fragment VIII is derived from the 3rd. exon of the nov gene;
CC nucleotide sequences which hybridise to Fragment VIII under stringent
CC conditions (i.e. 50% formamide, 5 x SCC) are claimed. The claimed
CC sequences preferably encode a protein with at least 70% homology to
CC R31602 which is encoded by Fragment VIII.
SQ Sequence 252 BP; 43 A; 76 C; 88 G; 45 T;

DB	6;	Score	106;	Match	77.0%;	QryMatch	5.1%;	Pred. No.	1.64e-41;
Matches	151;	Conservative	0;	Mismatches	45;	Indels	0;	Gaps	0;

Db	18	ctgcgtgttcgatgggatgattacgcgaacggggagacgttccagccagctgcaagta	77
Qy	435	CTGCATCTTCGGTGTACGGTGTAACCGACGGAGAGTCCCTTCACAGCAGCTGCAAGTA	494
Db	78	ccagtgcacctgccgggacgggcagatcggtgcctgccccgctgcacctgggcctgct	137
Qy	495	CCACTGCACGTGCCTGGACGGGGGGTGGGCTGCATGCCCCCTGTGCAGATGGACGTTTCG	554
Db	138	gtctccccggccccgactgcaccttccccgggaagatcgaagtcctcccgagagtgctgcga	197
Qy	555	TCTGCCCAGCCCTGACTGCCCTTCCCGAGGAGGGTCAAGCTGCCCGGAAAATGCTGCGA	614
Db	198	gaagtgggtgtgcgac	213
Qy	615	GGACTGGGTGTGTGCAC	630


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RESULT 7
ID Q36045 standard; cDNA; 196 BP.
AC Q36045;
DT 24-MAY-1993 (first entry)
DE Chicken nov gene exon 3 fragment XXIV.
KW avian nephroblastoma; avian myeloblastoma virus;
KW stringent hybridisation; ss.
OS Gallus domesticus.
PN W09300430-A.
PD 07-JAN-1993.
PF 25-JUN-1992; F00589.
PR 25-JUN-1991; FR-007807.
PA (CNRS) CENT NAT RECH SCI.
PI Martinerie C, Perbal B;
DR WPI; 93-036377/04.
PT Nucleotide sequences hybridising to regions of chicken nov gene -
PT useful as probes for detecting complementary sequences to
PT evaluate development and/or differentiation of tumours
PT Claim 24; Page 40; 67pp; French.
CC The chicken nov gene is stimulated in avian nephroblastoma induced
CC by avian myeloblastoma virus but not in normal adult kidney. A
CC 1975bp cDNA sequence (Q36031) was isolated from a gene bank prepared
CC from chicken embryonic fibroblasts screened with a tumour-derived
CC probe. Fragment XXIV (Q36045) is part of the 3rd exon of the nov gene;
CC nucleotide sequences which hybridise to Fragment XXIV under stringent
CC conditions (i.e. 50% formamide, 5 x SCC) are claimed. (N.B. the
CC sequence XXIV is described as an amino acid sequence in the claims
CC but is described correctly in the disclosure).
CC Sequence 196 BP; 32 A; 65 C; 66 G; 33 T;

DB 6; Score 106; Match 77.0%; QryMatch 5.1%; Pred. No. 1.64e-41;
Matches 151; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1 ctgcgtgttcgatggatgattaccgcgaacggggagacgttccagcccagctgcaagta 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 435 CTGCATCTTCGGTGTACGGTGTACCGCAGCGGAGAGTCTCTCCAGACGACTGCAAGTA 494

Db 61 ccagtgccactgcgggacgggcagatcggtgtcctgccccgcgtgcaacctgggcctgct 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 495 CCAGTGCACGTGCCTGGACGGGGGGTGGGCTGCATGCCCTGTGCAGCATGGACGTTCCG 554

Db 121 gtcctccggccccgactgccccctcccgcggaagatcgaagtcctcccgagagtgctgcga 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 555 TCTGCCACGCCCTGACTGCCCTTCCCGAGGAGGGTCAAGCTGCCCGGGAAATGCTGCCGA 614

Db 181 gaagtgggtgtgcgac 196
| ||||| ||||| ||||
Qy 615 GGAGTGGGTGTGTGAC 630

RESULT 8
ID Q36049 standard; DNA; 131 BP.
AC Q36049;
DT 24-MAY-1993 (first entry)
DE Fragment XXVII encodes protein homologous to chicken nov protein.
KW avian nephroblastoma; avian myeloblastoma virus;
KW stringent hybridisation.
OS Homo sapiens.
PN W09300430-A.
PD 07-JAN-1993.
PF 25-JUN-1992; F00589.
PR 25-JUN-1991; FR-007807.

```

PA	(CNRS) CENT NAT RECH SCI.
PI	Martinerie C, Perbal B;
DR	WPI; 93-036377/04.
PT	Nucleotide sequences hybridising to regions of chicken nov gene -
PT	useful as probes for detecting complementary sequences to
PT	evaluate development and/or differentiation of tumours
PS	Disclosure; Page 42; 67pp; French.
CC	The invention includes nucleotide sequences which encode amino acid
CC	sequences with at least 80% homology to sequence XXX (R31611), i.e
CC	to part of the chicken nov protein encoded by the 4th. exon. Such
CC	sequences preferably encode the amino acid sequence XXXI (R31612)
CC	and have the nucleotide sequence XXII.
SQ	Sequence 131 BP; 30 A; 40 C; 35 G; 26 T;
DB 6; Score 103; Match 95.6%; QryMatch 5.0%; Pred. No. 7.54e-40; Matches 129; Conservative 0; Mismatches 2; Indels 4; Gaps 2;	
Dbl	1 ctgtctcgcagctaccgactgggaacacagtgttgcccgagacccaactatgattag 60
Qy	659 CTGCCCTCGGGCTTACCGACTGGAACACAGCCTTGCCCCAGACCCTATGATTAG 718
Dbl	61 ccaac---ctggttcagac-acagaatggagcctgttcccagacctgtggatgggca 116
Qy	719 CCAACTGCCTGTGTCAGACACAGACTGGAGGCCCTGTCCAAGACCTGTGGGATGGCA 778
Dbl	117 tctccaccgggta 131
Qy	779 TCCTCACCCGGTTA 793
RESULT 9	
ID	Q26421 standard; cdna; 2028 BP.
AC	Q26421;
DT	18-JAN-1993 (first entry)
DE	Gene for beta-IG-M1.
KW	Transforming growth factor beta; induced; CEF-10; v-src; chicken;
KW	embryo; fibroblasts; TGF-beta; ss.
OS	Mus musculus.
FH	Key Location/Qualifiers
FT	CDS 186..1322
FT	/**tag= a
PN	EP-495674-A.
PD	22-JUL-1992.
PF	17-JAN-1992; 300429.
PR	18-JAN-1991; US-642991.
PR	10-JAN-1992; US-816270.
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
PI	Brunner AM, Chinn J, Neubauer MG, Purchio AF;
DR	WPI; 92-243508/30.
DR	P-PADB; R25565.
PT	TGF-beta induced gene family - encodes proteins involved in
PT	growth and differentiation effects of TGF-beta-1
PS	Claim 6; Fig 1; 35pp; English.
CC	The DNA encoding mouse beta-IG-M1 was obtd. from AKR-2B mouse cells
CC	induced with TGF-beta1 and cyclohexamide. Poly RNA extracted from
CC	these cells was used to create a cDNA library which was screened
CC	using two probes. The probes were prepd. from untreated AKR-2B mRNA
CC	and AKR-2B mRNA from cells treated with cyclohexamide and TGF-beta1.
CC	Hybridising colonies were isolated and two clones (beta-IG-M1 and
CC	beta-IG-M2) were then sequenced. The DNA encodes proteins that
CC	have a 80 and 50 percent homology respectively with the CEF-10
CC	protein induced by v-src in chicken embryo fibroblasts. The
CC	proteins encoded by TGF-beta induced genes are likely to be
CC	involved in mediation of the biological effects of TGF-beta

Qy	632	AGCCCAAGCACCAACCGTGGTTGGGCCTGCGCCTCGCGGCTTACCGACTGGAACACACCT	691
Db	665	naenrstannddnnanyakknntannnnsgnnnttgmnaadvysngnnnnnnnansrgnn	724
Qy	692	TTGGCCCGACAGCCCAACTATGATTAGAGCCAACTGCGCTGGTCCAGACCACAGAGTGGAGCG	751
Db	725	ynngndhanknnvkvrngnrnynrnsndrtnnnnnvnnnmnrnwandnandrndngnnkg	784
Qy	752	CCTGTTCCAAGACCTG-TGGGATGGGCACTCTCCACCCGGGTTACCAATGACAAACGCCCTCC	810
Db	785	nnrrnnkngtssnddnnnmnmnyannnnknvnnrtnaynnnnkrkanannynnnnhsvan	844
Qy	811	TGCAGGCTAGAGAAGCAGAGCCGC-CTGTGCATGGTCAGGCCCTTCCGAAGCTGACCTGGA	869
Db	845	nnkrgntvnandsvtnynsdhvgntansanstmnnvvtnnndnytcndannndndvyk	904
Qy	870	AGAGAACATTAGAAGGGCAAAAGTGCACTCCGTACTCCCAAAATCTCCAAGCCTATCAA	929
Db	905	vntngdaymvvsngngrnhrhannarmanandavssnrnrhrhndnrrnrgvh-tg	963
Qy	930	GTTTGAGCTTTCTGGCTGCACACGATGAACACATACCGAGCTAAATCTGTGGAGTATG	989
Db	964	nvcagvvgknmrycnngdtvntaermnsngnanknhvssttkdandngcnnnnnrgdv	1023
Qy	990	TACCGAGCGCGGATGCTGCACCCCCACAGAACCAACACCCCTGCCCGGTGGAGTTCAAGTG	1049
Db	1024	nm 1025	
Qy	1050	CC 1051	
RESULT 11			
ID	Q10572	standard; DNA; 1047 BP.	
AC	Q10572;		
DT	09-APR-1991	(first entry)	
DE	Human Natriuretic Peptide Receptor B.		
KW	NPBR; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;		
KW	hyperaldosteronism; glaucoma; guanyl cyclase.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..22	
FT	/label=	signal sequence	
FT	Protein	12	
FT	/label=	mature NPBR	
FT	Domain	23..455	
FT	/label=	extracellular domain	
FT	/note=	"binds natriuretic peptides A, B and C]"	
FT	Domain	456..456	
FT	/label=	transmembrane domain	
FT	Domain	479..1047	
FT	/label=	cytoplasmic domain	
FT	/note=	"GC and protien kinase activity"	
FT	Modified -site	24..26	
FT	/label=	N-glycos site	
FT	Modified -site	35..37	
FT	/label=	N-glycos site	
FT	Modified -site	161..163	
FT	/label=	N-glycos site	
FT	Modified -site	195..197	
FT	/label=	N-glycos site	
FT	Modified -site	244..246	
FT	/label=	N-glycos site	
FT	Modified -site	277..279	
FT	/label=	N-glycos_site	

FT	Modified -site	349..351	
FT	/label=	N-glycos_site	
FT	Modified -site	600..602	
FT	/label=	N-glycos_site	
PN	WO9100292-A.		
PD	10-JAN-1991.		
PF	22-JUN-1990; U03586.		
PR	23-JUN-1989; US-370673.		
PA	(GETH) GENENTECH INC.		
PI	Chang M, Goeddel D, Lowe D;		
DR	WPI; 91-036711/05.		
DR	N-PSDB; Q10324.		
PT	Natriuretic protein receptor B - for diagnosis and treatment of		
PT	kidney failure, heart failure, hyperaldosteronism, glaucoma etc.		
PS	Claim 3; Fig 1; 49pp; English.		
CC	The sequence was derived from the DNA encoding natriuretic peptide		
CC	receptor B, NPBR, having guanyl cyclase (GC) activity and protein		
CC	kinase activity. The DNA can be inserted into expression vectors		
CC	for the prodn. of the protein, opt. after being mutated to produce		
CC	NPBR analogues. The protein has a mol wt. of 115 kD (calculated Mr=		
CC	114,952). The protein (or variante) can be used in treatment of		
CC	natriuretic peptide disorders, and also to isolate peptides using		
CC	affinity chromatography. Antibodies with affinity for NPBR can		
CC	also be prepd.		
SQ	Sequence	1047 BP; 87 A; 15 C; 83 G; 51 T;	
DB 2; Score 79; Match 9.1%; QryMatch 3.8%; Pred. No. 9.36e-27;			
Matches 86; Conservative 270; Mismatches 578; Indels 13; Gaps 12;			
Db	85	vdnknyhdnngngcvynaasvarnashwrnnnnntagavagsnsakndhyrtnvrtgn	144
Cp	970	CTCGGTATGCTTTCATGCTGCTGCAGCCAGAAAGCTCAAAC TTGATAGGCTTGAGATTT	911
Db	145	sankngmvvtnhghnnwtaraannnyndartddrhnvntnngvnnannsgnsvnhnvya	204
Cp	910	TGGAGTAGCGATGCACATTTTTCGCCCTCTTTAAATGTTCTCTCCAGGTCAGCTTCGCAAG	851
Db	205	rnnggnnnathnnrangrnrvnvcgnnnmmhnnnnnannrnnntngdyvnnynndvngnsnra	264
Cp	850	GCCTGACCATGCACAGGCGGCTCTGCTTCTTAGCCCTGCAGAGGCGTTGTCTAFTGGTAA	791
Db	265	gntratgrnwndnrtrnnananrnanntvntvtnrnnnnnnnnnnnnnnnnrnrarndngvn	324
Cp	790	CCCG--GGTGGAGATGCCCATCCACAGGCTCTTGAACAGGCGCTCCACTCT-GTGGTCT	734
Db	325	ngnsnmnnagcnydgnnnyanvnnntnnngqtrndgrnrvnkmgrryhgvtgnvmdk	384
Cp	733	GGACCAGGCAG-TTGGCTCTAATCATAGTTGGGTCTGGGCCCAAACGTGTCTTCAGTCCG	675
Db	385	nndrntdvnwamgdndsgdhnnnaahysganknnwTgrnnnwkvgnnsdhnnncandnd	444
Cp	674	TAAGCGCGCAGGCGAGGCCCAACCAACGCTTTGGTCTCTGGGTCCGTACACACCCACTCC	615
Db	445	dnscdktnnstnnavngtgnntnnmgvssnnnnrknmmnknmmasmwrrn-rwnnnnnngn	503
Cp	614	TCGAGCATTTCCCGGCAGCTTGACCTCTCCTCGGGAAGGGCAGTCAGGCTGGGCAGA	555
Db	504	snryhkgagerntnenrgsygsnmtahgkynnnnantghknvvnvankhvnkkrnnntrn	563
Cp	554	CGAACGTCCATGCTGCACAGGGGCATGCAGCCACCCGCCCTCCAGGACGTCGACTG-	496
Db	564	vnnnnkhmrdrvnnnhntrnnngacndnnnnnenvtnycnrgsnndnnnnndwmnrysn	623
Cp	495	GTACTTGCAGCTGCTCTGGA-AGGACTCTCCGCTGCGGTACACCGTACCCGAAGATGC	437

624 nndnkvmanhnhsnnshgsknsncvvdrrnvknkntdygnasnrstannddnnanyak 683
 : :: : : :::: : |::| : : : :
436 AGGAGCACCATCTTTGGCGG-TGCACACGCCGATCTTCGGGTGGCCGGGAGCCGAAG 378
 : :: : : :::: : |::| : : : :
684 knntanhnsgnnnttgmaadvysngnnnnnanrsgnnyngndhnsknnvnkvrng 743
 : | |||| :::: : |::| : : : :
377 TCACAGAAGAGCCCCTTTCGGGGTGCGAGGGGTGGGCTCGGTGCACAGCTCGCCCCAGC 318
 : : : : : : : : : : : : : : : :
744 nrnyrnrsndrtnnnnnnvvnmrcwandhanrdngnkgnrirnnkngtssndnnnn 803
 : : : : : : : : : : : : : : : :
317 TGCTTGGGGCAGACGGCGGACGAGCGCGCGG-TCCAGCACAGAGGTCACGCCGCCGGC 259
 : : : : : : : : : : : : : : : :
804 rmannyannnnkvnnrtnaynnnnkrkanannynnnnhsvannnkrgntvnananandsvtuy 863
 : : : : : : : : : : : : : : : :
258 GCAGCGCGCGCGCGCTCGTCCGGGACC GGACGGCCCGCTGCAGTTCTTGGCGCAGCGC 199
 : : : : : : : : : : : : : : : :
864 nsdnvgntansan-stnmrvttnnndnytcdann-dnndvykvtngdaymv-vs-gnn 919
 : : | : : : : : : : : : : : : : : : :
198 CGGCCGCTGCAGAGGGCGAGGACCAACAGGGCAGCGGACGGGCCCCATACTGGC 139
 : : : : : : : : : : : : : : : :
920 grngnrhannnarmanandavssnrnrhrhndnrnrngvhtgnvcagvvgnkmmrycn 979
 | : | : : : : : : : : : : : : : : : :
138 GCGCGTCATGCTTGGCATCTCGCGGGGAGCGGAGGGCGCGCTGGCGCGCAGCGGGGAGCG 79
 : : : : : : : : : : : : : : : :
980 ngdvtntasrmnsngnanknhvssttkdandngcnnnnnrqdvnmk 1026
 | : : : : : : : : : : : : : : : :
78 CCGGGCCCTGCAGCGCTGGCGGTGTCTCGGAGGTGGGGACCGGAGCGG 32

RESULT	12	
ID	Q57417	standard; cDNA to mRNA; 372 BP.
AC	Q57417;	
DT	19-OCT-1994	(first entry)
DE	CYR61	like protein.
KW	Human cDNA;	library; enzyme; protein; ss.
OS	Homo sapiens.	
PN	W09403599-A.	
PD	17-FEB-1994.	
PF	04-AUG-1993;	J01095.
PR	04-AUG-1992;	JP-208077.
PR	13-NOV-1992;	JP-327619.
PR	26-FEB-1993;	JP-061431.
PA	(SAGA)	SAGAMI CHEM RES CENTRE.
PI	Iwahori A,	Kato S, Kato T, Kim N, Oh S, Sekine S;
DR	WPI;	94-065688/08.
DR	P-PSDB;	R46078.
PT	cDNA of	human origin and proteins coded by it - which may be
PT	expressed	by in vivo or in vitro translation using sense RNA or
PT	antisense	DNA corresponding to the cDNA.
PS	Claim 1;	Page 32-33; 167pp; Japanese.
CC	mRNA	expressed in human fibrosarcoma cell line HT-1080 was
CC	isolated	and used to construct a cDNA library using vector
CC	pKA1.	Clone HP00021 encoding CYR61-like protein
CC	was	isolated.
SQ	Sequence	372 BP; 93 A; 95 C; 107 G; 77 T;

DB 10; Score	67; Match 68.9%; QryMatch 3.2%; Pred. No. 2.18e-20;
Matches 122;	Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Db 70 taccaaaacgggaaagtgttccagccccactgtaaacatcagtgcacatgatgatgcg 129
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qw 457 TACCGCAGCGGAGAGTCTTCACAGCAGGTGCCAAGTACCAGTGCCAGTGCCTGCACGGG 516

Db	130	gcgctggctgcattcctctgtgtccccaagaactatctctcccaacttgggtgtccc	189
Qy	517	GCGGTGGCTGCATGCCCTGTGCACCATGACGCTCGTCTGCCAGCCCTGACTGCCCC	576
Db	190	aaccctcggtcgtcaaaagtaccggggcagtctgcgaggagtggtctgtgacgag	246
Qy	577	TTCCCGAGGAGGTCAAGCTGCCGGGAAATGCTGCAGGAGTGGTGTGTGACGAG	633

RESULT 13

ID Q36039 standard; cDNA; 216 BP.

AC Q36039;

DT 24-MAY-1993 (first entry)

DE Homologous to exon 3 of CTGF gene.

KW avian nephroblastoma; avian myeloblastoma virus;

KW stringent hybridisation; ss.

PN WO9300430-A.

PD 07-JAN-1993.

PF 25-JUN-1992; F00589.

PR 25-JUN-1991; FR-007807.

PA (CNRS) CENT NAT RECH SCI.

PI Martinerie C, Perbal B;

DR WPI; 93-036377/04.

DR P-PSDB; R31605.

PT Nucleotide sequences hybridising to regions of chicken nov gene -

PT useful as probes for detecting complementary sequences to

PT evaluate development and/or differentiation of tumours

PS Claim 14; Page 34; 67pp; French.

CC This sequence is homologous to exon 3 of the CTGF gene and was used

CC as a probe in Northern hybridisations with different human tissues

CC and cell lines. Probes homologous to exon 2 of the chicken nov gene

CC and to exon 4 of the CTGF gene (Q36035 and Q36040, respectively)

CC were also used in the hybridisation experiments. The results showed

CC that the human homologue of the chicken nov gene and the CTGF gene

CC belonging to the same family are expressed differently in different

CC tissues or lines as different RNA transcripts.

SQ Sequence 216 BP; 62 A; 56 C; 60 G; 38 T;

DB 6; Score 65; Match .67.2%; QryMatch 3.1%; Pred. No. 2.43e-19; Matches 127; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Db	1	ggttacagggccagaagcaccctaggagtagaagtctctgactcaagtgtcaactgcatt	60
Qy	670	GCTTACCACACTGGAGACACGTTTGCCCCAGACCCCACTATGATTAGAGCCAAC TGCTG	729
Db	61	gaacagaccacagagtggaacgatgctccaagagctgtgatatgggttctccacccgg	120
Qy	730	GTCCAGACCACAGAGTGGAGCGCCTGTTCCAAGACCTGTGGCATGGGCATCTCCACCCGG	789
Db	121	gtcaccaataggaaacctgaatgtgagatgctgaacagagctcggtctctgcatagtgcgg	180
Qy	790	GTTACCAATGACAACGCCCTCTCTGCAGGCTACAGAAGCAGAGCGCGCTGTGCATG	849
Db	181	ccctgtgaa	189
Qy	850	CCTTCGGAA	858

RESULT 14
ID Q36040 standard; cDNA: 435 BP.

DT 24-MAY-1993 (first entry)
DE Homologous to exon 4 of CTGF gene.
KW avian nephroblastoma; avian mveloblastoma virus;

WIREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Fri Sep 22 21:58:20 1995; MasPar time 1084.25 Seconds
Tabular output not generated. 1117.032 Million cell updates/sec

Title: >US-08-167-628-1
Description: (1:2075) from 5408040.seq
Perfect Score: 2075
N.A. Sequence: 1 CCCGGCGGACACCCCGCAGA.....AGGAATGTGGTAGCTCAGC 2075
Comp: GGGCGGCTGTGGGGCTCT.....TCCTTACACCATCGAGTGC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 267821 seqs, 291840210 bases x 2

Database: embl-new6

- 1 BCT
- 2 EST1
- 3 EST2
- 4 EST3
- 5 EST4
- 6 EST5
- 7 FUN
- 8 INV1
- 9 INV2
- 10 MAM
- 11 ORG
- 12 PLN
- 13 PRI
- 14 PRO
- 15 ROD
- 16 STS
- 17 SYN
- 18 UNC
- 19 VRT
- 20 VIR

Database: genbank89
21 BCT1
22 BCT2
23 BCT3
24 BCT4
25 BCT5

- 26 BCT6
- 27 INV1
- 28 INV2
- 29 INV3
- 30 INV4
- 31 INV5
- 32 MAM1
- 33 MAM2
- 34 PAT1
- 35 PAT2
- 36 PHG
- 37 PLN1
- 38 PLN2
- 39 PLN3
- 40 PLN4
- 41 PLN5
- 42 PLN6
- 43 PLN7
- 44 PRI1
- 45 PRI2
- 46 PRI3
- 47 PRI4
- 48 PRI5
- 49 PRI6
- 50 PRI7
- 51 PRI8
- 52 PRI9
- 53 ROD1
- 54 ROD2
- 55 ROD3
- 56 ROD4
- 57 ROD5
- 58 ROD6
- 59 ROD7
- 60 STR
- 61 STS1
- 62 STS2
- 63 STS3
- 64 STS4
- 65 SYN
- 66 UNA
- 67 VRL1
- 68 VRL2
- 69 VRL3
- 70 VRL4
- 71 VRL5
- 72 VRL6
- 73 VRT1
- 74 VRT2
- 75 VRT3

Database: genbank-new6

- 76 BCT
- 77 EST1
- 78 EST2
- 79 EST3
- 80 EST4
- 81 EST5
- 82 EST6
- 83 EST7
- 84 EST8
- 85 INV
- 86 MAM
- 87 PHG

88 PLN

89 PRI

90 ROD

91 STS

92 STR

93 SYN

94 UNA

95 VRL

96 VRT

Database:

u-embl43 89

97 ALL

Statistics:

Mean 12.417; Variance 7.139; scale 1.739

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2075	100.0	2075	48	HUMCONGRO	Human connective tiss	0.00e+00
2	2075	100.0	2075	52	S56201	connective tissue gro	0.00e+00
3	2022	97.4	2312	44	HSCTGF	H.sapiens mRNA for co	0.00e+00
4	921	44.4	2330	57	MUSTGFB	Mouse mRNA sequence.	0.00e+00
5	909	43.8	2267	55	MUSFISP12B	Mouse FISP-12 protein	0.00e+00
6	354	17.1	4128	55	MUSFISP12A	Mouse FISP-12 protein	4.05e-224
7	264	12.7	1976	74	GGNOVMRNA	G.gallus nov mRNA.	9.46e-159
8	252	12.1	1927	73	CJU13063	Coturnix japonica cel	4.22e-150
9	127	6.1	1805	73	CHKCEF	Chicken CEF-10 protei	8.80e-62
10	88	4.2	2018	55	MUSCYR61A	Mouse Cyr61 mRNA, com	1.39e-35
11	68	3.3	1469	46	HSNOVH5	H.sapiens novH gene e	9.25e-23
12	65	3.1	435	46	HSNOVH4	H.sapiens novH gene e	6.81e-21
13	62	3.0	452	46	HSNOVH3	H.sapiens novH gene e	4.80e-19
14	60	2.9	5196	53	MMCYR61G	Mouse growth factor i	7.98e-18
15	52	2.5	557	46	HSNOVH12	H.sapiens novH gene e	4.80e-13
16	44	2.1	226	86	BTMSAT90	B.taurus microsatelli	1.79e-08
17	44	2.1	226	10	BTMSAT90	B.taurus microsatelli	1.79e-08
18	43	2.1	261	63	HS154XC7	H. sapiens (DIS216) D	6.41e-08
19	42	2.0	221	33	SHPMAF4P	Ovis aries dinucleoti	2.27e-07
20	41	2.0	322	63	HUM4STS367	Human chromosome 4 se	7.93e-07
21	41	2.0	392	33	SSMIC	S.scrofa pseudogene c	7.93e-07
22	41	2.0	499	63	HUM4STS439	Human chromosome 4 se	7.93e-07
23	40	1.9	184	53	MMD3NDS3	M.musculus D3nds3 mic	2.74e-06
24	40	1.9	365	63	HS345WH9	H. sapiens (D4S1617)	2.74e-06
25	40	1.9	340	62	HS116XG1	H. sapiens (DXS986) D	2.74e-06
26	40	1.9	163	62	GGU23939	Gorilla gorilla dinuc	2.74e-06
27	40	1.9	260	79	R72445	yJ90h07.s1 Homo sapie	2.74e-06
28	40	1.9	353	63	HS248WC5	H. sapiens (D2S172) D	2.74e-06
29	40	1.9	146	51	HUMVTR14K	Human variable tandem	2.74e-06
30	40	1.9	1782	55	MUSATP4B1	Mouse gastric (H+,K+)	2.74e-06
31	40	1.9	418	33	SS13N06R	S.scrofa genomic DNA	2.74e-06
32	40	1.9	397	32	BTMSINRBN	B.taurus microsatelli	2.74e-06
33	39	1.9	669	47	HSU19800	Human m2 muscarinic a	9.36e-06
34	39	1.9	3578	13	HSLOD3	Human lysyl hydroxyla	9.36e-06
35	39	1.9	387	63	HUM4STS237	Human chromosome 4 se	9.36e-06
36	39	1.9	354	51	HUMSIRPOBN	Human simple repeat p	9.36e-06
37	39	1.9	3578	46	HSPLOD3	Human lysyl hydroxyla	9.36e-06
38	39	1.9	529	64	HUMUT5046	Human STS UT5046.	9.36e-06
39	39	1.9	407	64	HUMUT454	Human chromosome 8 ST	9.36e-06
40	39	1.9	8633	30	PFPFMDR1	P.falciiparum pfmdri g	9.36e-06

41	39	1.9	3578	89	HSPL0D3	Human lysyl hydroxyla	9.36e-06
42	39	1.9	609	64	HUMUT866	Human chromosome 2 ST	9.36e-06
43	39	1.9	328	63	HS196XB4	H. sapiens (DIS228) D	9.36e-06
44	38	1.8	187	51	HUMRPTPOLE	Human repeat polymorp	3.16e-05
45	38	1.8	192	48	HUMCHR8F	Human chromosome 8 DN	3.16e-05

ALIGNMENTS

RESULT 1

LOCUS HUMCONGRO 2075 bp mRNA PRI 30-APR-1992

DEFINITION Human connective tissue growth factor, complete cds.

ACCESSION M92934 M36965

KEYWORDS growth factor; mitogen.

SOURCE Homo sapiens (library: lambda gt11) connective cDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

REFERENCE 1 (bases 1 to 2075)

AUTHORS Bradham,D.M., Igarashi,A., Potter,R.L. and Grotendorst,G.R.

TITLE Connective tissue growth factor: a cysteine-rich mitogen secreted by human vascular endothelial cells is related to the SRC indeuced immediate early gene product CEF-10

JOURNAL J. Cell Biol. 114, 1285-1294 (1991)

MEDLINE 91373462

COMMENT NCBI gi: 180923

FEATURES Location/Qualifiers

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Matches 2075; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ccagcgctccagccccggctcccgctccgcccaccgcccctccgctccgcccga 120

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QY 61 CCAGCGCTCCAGGGCCCGCGCTCCCGCTCCCGCCGACCGGCCCTCCGCTCCGCCCGCGCA 120

Db 121 gtgccaaacatgaccgccgcagatgggcccctgcgcgctccgccttcgtggtccctc 180
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Db 181 gccctctgcagccgccgcgctcgccagaaactgaagcgggcgctgcgcggtgccccgac 240
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Db 241 gaagccggcgcgcgctgccgcggcggtgagccctcgtgctgacggcgtgcgctgtgc 300
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Qy 2041 GGCTGATTCTTAGGTAGGAAATGTGTTAGTCAAG 2075

RESULT 2
LOCUS S56201 2075 bp mRNA PRI 29-APR-1993
DEFINITION connective tissue growth factor [human, umbilical vein endothelial
cells, mRNA, 2075 nt].
ACCESSION S56201
KEYWORDS .
SOURCE human umbilical vein endothelial cells.
ORGANISM Homo sapiens
Unclassified.
REFERENCE 1 (bases 1 to 2075)
AUTHORS Igarashi,A., Bradham,D.M., Okochi,H. and Grotendorst,G.R.
TITLE Connective tissue growth factor
JOURNAL. Journal of Dermatology 19 (11), 642-643 (1992)
MEDLINE 93187114
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 127024] from the original journal article.
This sequence comes from Fig. 1.
COMMENT NCBI gi: 266234
FEATURES
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Matches 2075; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2041 GCCTGATTTCTAGGTAGGAAATGTGCTAGCTCAGC 2075

RESULT 3

LOCUS HSC7GF 2312 bp RNA PRI 25-APR-1994

DEFINITION H.sapiens mRNA for connective tissue growth factor.

ACCESSION X78947

KEYWORDS connective tissue; growth factor.

SOURCE human.

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 2312)
Oemar,B.S., Werner,A., Yang,Z., Garnier,J.M., Gentz,R. and
Luescher,T.F.
Differential cloning and expression of human connective tissue
growth factor
Unpublished
2 (bases 1 to 2312)
Oemar,B.S.
Direct Submission
Submitted (22-APR-1994) to the EMBL/GenBank/DBJ databases. B.S.
Oemar, University Hospital Basel, Dept of Research, Lab of Vascular
Research, Hebelstr. 20, 4031 Basel, SWITZERLAND
NCBI gi: 474933
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BASE COUNT 572 a 594 c 585 g 561 t
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Db 77 ccagcgtccagcccccgctcccgctcccgccacccgcgccctccgctccgcccga 136
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Qy 61 CCAGCGCTCAGGCCCGCGCTCCCGCTCCCGCCAGCCGCGCCCTCGCTCCGCCGCCA 120

Db 137 gtgccaaaccatgaccgcccagtatggccccgtcgcgctgcgttcgtgctcctc 196
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Qy 121 GTGCCAACCATGACCGCCGACGATATGGCCCGGTCCCGTCCGCTTGGTGTCTCTC 180

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Db	257	gagccggcgccgcctgcccggcgggcgctgcagcctcgtgctgcagcggctgcgcgtgtgc	316
Qy	241	GAGCGGCGCGCGCTGCCGGCGGCGTGAGCCTCGTGTGCACGGCTGCGGTGCTGC	300
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Qy	301	CGCGTCTCGGCCAAAGCAGCTGGCGAGCTGTGCACCGCGGACCCCTGCGACCGGAC	360
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Qy	361	AAGGGCCTTCTCTGACTTCGGCTCCCGGCCCAACCGCAAGATCGGCGTGTGCACCGCC	420
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Qy	421	AAAGATGTFGCTCCCTGCATCTTCGGTGGTACGGGTACCGAGCGGAGAGTCTCTCCAG	480
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Db	617	gggaatatgctgcgaggagtgggtgtgtgacgagcccaaggacaaaaccgtggtggccct	676
Qy	601	GGGAATGCTCGGAGGAGTGGGTGTGTGACGAGCCCAAGGACCAACCGTGGTGGGCT	660
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Qy	661	GCCTCGCGGCTTACCGACTGGAAGACACGTTTGGCCAGACCCCAACTATGATTAGAGCC	720
Db	737	aactgcctggtccagaccacagagtggagcgctgttccaagacctgtgggtgggcac	796
Qy	721	AACTGCCTGTTCCAGACCACAGAGTGGAGCGCTGTTCCAAGACCTGTGGATGGGCATC	780
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Qy	781	TCCACCGGGTTACCAATGACAACGCTCTCTCAGGCTAGAGAAGCAGAGCCGCGTGTGC	840
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Qy	901	CGTACTCCCAAAATCTCCAAGCCTATCAAGTTTGAGCTTCTGGCTGCGCAGCATGAAG	960
Db	977	acataccgagctaaattctcgaagcctatgacccgaecgcgatgctgcacccccacaga	1036
Qy	961	ACATACCAGCTAAATTCTGTGGAGTATGTACCGAGCGCGGATGCTGCACCCCCACAGA	1020
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Qy	1021	ACCACACCCCTGCCGTTGGAGTTCAAGTGCCCTGACGGGAGTCTATGAAGAACAATG	1080
Db	1097	atgttcataaagacctgtgcctgccattacaactgtcccgagagacaatgacatctttgaa	1156
Qy	1081	ATGTTCAACAAGACCTGTGCCTGCCATTACAACGTGTCCGGAGACAATGACATCTTTGAA	1140

Db	1157	tcgctgtactacaggaagatgtacggagagaatggcatgaagccagagagtgagagacatt	1216
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Qy	1558	CCTGCCTGTAGCCCGAGTGACAGCTAGGATGCTGCA TTCTCCAGCCATCAAGAGACTGACT	1617
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Qy	1858	TTTTGTTTTTAATGCTTTGATATTTCAA TGTAGCCTCAA TTCTGAACCATAGGTAG	1917
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Qy	1918	AATGTAAAGCTTGTCTGATCGTTCAAAGCATGAAATGGATACTTATATGAAAATTCGCT	1977
Db	1994	cagatagaatgacagtcggtcaaaacagattgtttgaaaaggggaggaatcagtgctcct	2053
Qy	1978	CAGATAGAATGACACTCCGTCAAACACAGATTGTTTGC AAAGGGGAGGCATCACTGTC-TT	2036
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Qy	2037	GGCAGGCTGATTTCTAGGTAGGAAAATGTGTAGTCAAG	2075


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RESULT      4
LOCUS      MUSTGFB      2330 bp      mRNA      ROD      01-NOV-1991
DEFINITION      Mouse mRNA sequence.
ACCESSION      M80263
KEYWORDS      transforming growth factor-beta.
SOURCE      Mus musculus cDNA to mRNA.
ORGANISM      Mus musculus
              Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
              Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE      1 (bases 1 to 2330)
AUTHORS      Brunner,A., Chinn,J., Neubauer,M.G. and Purchio,A.F.
TITLE      Identification of a gene family regulated by transforming growth
              factor-beta
JOURNAL      DNA Cell Biol. 10, 293-300 (1991)
MEDLINE      91229699
COMMENT      NCBI gi: 201945
FEATURES      Location/Qualifiers
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Db

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230 GGTGCCCGGACAGCCGGCCCCGCCTGCCCGGGGGCCTGACCCTCGTCTCGA CCGCT 289

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Oy			

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Qy	530	TGCCCCCTGTGCAGCATGGACGTTCTGTCTGCCCAAGCCCTGACTGCCCTTCCCAGAGGGG	589
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Qy	590	TCAAGCTGCGCGGAAATGCTCGGAGGAGTGGTGTGTGTACGAGCCCAAGGACCAAAACCG	649
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RESULT 6

LOCUS MUSFISP12A 4128 bp DNA ROD 09-JUL-1991

DEFINITION Mouse FISP-12 protein (fisp-12) gene, complete cds.

ACCESSION M70641

KEYWORDS cysteine-rich protein; growth factor-inducible gene.

SOURCE Mus musculus (sub_species domesticus) liver/kidney DNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 4128)

AUTHORS Ryseck, R.-P., MacDonald-Bravo, H., Mattei, M.-G. and Bravo, R.

TITLE Structure, mapping and expression of fisp-12, a growth factor inducible gene encoding a secreted cysteine-rich protein

JOURNAL Cell Growth Differ. 2, 225-233 (1991)

MEDLINE 91363290

COMMENT NCBI gi: 193313

FEATURES

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RESULT      7
LOCUS      GGNVOMRNA      1976 bp      RNA      VRT      08-JAN-1992
DEFINITION      G.gallus nov mRNA.
ACCESSION      X59284
KEYWORDS      NOV gene.
SOURCE      chicken.
ORGANISM      Gallus gallus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Reptilia; Sauria; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 1976)
AUTHORS      Perbal,B.
TITLE      Direct Submission
JOURNAL      Submitted (19-APR-1991) to the EMBL/GenBank/DBJ databases. B.
Perbal, Institut Curie, Centre Universitaire Batiment 110, 91405 -
Orsay, Cedex, FRANCE
REFERENCE      2 (bases 1 to 1976)
AUTHORS      Joliot,V., Martinerie,C., Dambrine,G., Plassiart,G., Brisac,M.,
Crochet,J. and Perbal,B.
TITLE      Proviral rearrangements and overexpression of a new cellular gene
(nov) in myeloblastosis-associated virus type 1-induced
nephroblastomas
JOURNAL      Mol. Cell. Biol. 12 (1), 10-21 (1992)
MEDLINE      92107157
COMMENT      NCBI gi: 63702
FEATURES      Location/Qualifiers
source      1..1976
/organism="Gallus gallus"
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/strain="Brown Leghorn"
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/cell_type="fibroblast"
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/clone="pClK"
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25..1080
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GECEKWCVDPRDEVLLGGFAMAA1RQEATLIGIDVSDSSANCIEQTTEWSACSKSCGM
GFSTRVTNRNQCEVMVKQTRLCMRPCENEEP3DKGKKCIQTKSKMAVRFEVKNCT
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322..573
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polyA_signal 1815..1820
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BASE COUNT 522 a 452 c 486 g 516 t
ORIGIN
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DB 74; Score 264; Match 66.0%; QryMatch 12.7%; Pred. No. 9.46e-159;
Matches 575; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

Db 152 cgcgcgctgcgcgcgggagtgccgcgctgctggacggtgcggctgctgctggtgt 211
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Qy 248 CGCGCGCTGCCCGGGGGGTGAGCCTCGTGTGTGAGCGGTGCGGCTGCTGCGCGCT 307

Db 212 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 271
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Qy 308 GCGCCAAGCAGCTGGCGGAGCTGTGCACCGGCGCGGACCCCTCGGACCCGCACAGGGCC 367

Db 272 tctactgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 331
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Qy 368 TCCTCTGTGACTTCGGCTCCCCGGCCAAACCCCAAGATCGGCGCTGTGCACCGCCAAAGATG 427

Db 332 gggacaaactgcgtgttcgatgggatgattaccgcgcgcgcgcgcgcgcgcgcgcgcgcgc 391
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Qy 428 GTGCTCCCTGCATCTTCGGTGGTACCGGTGTACCGGACGGAGAGTCTCTCCAGACGAGT 487

Db 392 gcaagtaccagtgccacctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 451
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Qy 488 GCAAGTACCAGTGCACGTGCCTGGACGGGGGGTGGGCTGCATGCCCTGTGCAGCATGG 547

Db 452 gctgctgctccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 511
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Qy 548 AGCTTCGTCTGCCAGACCCCTGACTGCCCCCTTCCCGAGGAGGCTCAAGCTGCCCGGGGAAAT 607

Db 512 gctgcgaagaagtgggtgtgcgacccaggggatgaagtgcctcctgggaggtttgctatgg 571
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Qy 608 GTCGAGGAGTGGGTGTGTACAGACCCCAAGGACCAACCGTGGTTGGGCTTGCCTCG 667

Db 572 ctgcatacacagaggaggccacacttggatagacgtgtctgatteaagtgccaaattgta 631
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Qy 668 CGGCTTACCGACTGGAAGACACGTTTGGCCCGAGACCCCAACTATGATTAGAGCCAACTGCC 727
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Db 632 ttgaacagacaagaatggagtgcttgtttcaaaagctgtggaatggcgttttctacc 691
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Qy 728 TGGTCCAGACCACAGATGGAGCGGCTGTTCCAGAGCTGTGGATGGGCATCTCCACCC 787

Db 692 gtgttaccacaagaatcagcagtgagatggtgaagcagacacgactttgcatgatga 751
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Qy 788 GGGTTACCAATGACAACGGCTCCTGCAGGCTAGAGAAGCAGAGCCCGCTGTGCATGGTCA 847

Db 752 gacctgtgaacagaagagcccatctga---taagaaggaataaatgtatccaaacaa 808
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Qy 848 GGCCTTGCGAAGCTGACCTGGAAGACAACATTAGAGAGGGCAAAAAGTCCATCCGTACTC 907

Db 809 agaaatcccatgaaagctgttcgttttgaatacaagaactgcaccagtgtcagacttaca 868
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Qy 908 CCAAAATCTCCAAGCCTATCAAGTTTGAGCTTCTGCTGCACCGCATGAAGACATACC 967

Db 869 aacctcgttactgtggcctctcgaatgatgggcgatggtaccacacacacacacaaa 928
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Qy 968 GAGCTAAATTCTGTGGAGTATGTACCGACGGCGCGATGCTGCACCCCGCACAGAACCCCA 1027

Db 929 cgattcaagttgagttccgctgtcctcaggcgaatcctaataaaagccaatgatgttga 988
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Qy 1028 CCCTGCCGGTGGAGTTCAAGTCCCTGACGGCGAGTCAATGAAGAAGAACATGATGTTCA 1087

Db 989 tcaatacctgtgtctgtcatggtaactgtcc 1019
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Qy 1088 TCAAGACCTGTGCCTGCCATTACAACTGTCC 1118
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RESULT 8
LOCUS CJU13063 1927 bp mRNA VRT 28-AUG-1994
DEFINITION Coturnix japonica cellular proto-oncogene protein Nov (nov) mRNA,
complete cds.
ACCESSION U13063
KEYWORDS .
SOURCE Coturnix japonica.
ORGANISM Coturnix japonica
Eukaryotae; Hyperchondria; Eukaryote crown group; Metazoa/Eumycota
group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia;
Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii;
Choanata; Tetrapoda; Amniota; Reptilia; Sauria; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
REFERENCE 1 (bases 1 to 1927)
AUTHORS Weiskirchen,R. and Bister,K.
TITLE Suppression in transformed avian fibroblasts of the nov
protooncogene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1927)
AUTHORS Bister,K.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-1994) Bister K., University of Innsbruck,
Institute of Biochemistry, Peter-Mayr-Strasse 1a, Innsbruck,
Austria, A-6020
COMMENT NCBI gi: 532696
FEATURES Location/Qualifiers
source
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/clone_lib="QEF cDNA library of R. Weiskirchen and K.
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/organism="Coturnix japonica"
/cell_type="fibroblast"
/dev_stage="embryo"
14..1075
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CDS
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Db 219 tgcgccaacgactgaacgagactgcagccgcagcgacgcagccctgcgaccacacacaaggagg 278
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Qy 307 TGCCCCAACGAGCTGGCGAGCTGTGCACCGAGCCGACCCCTGCCAGCCCGCACAAAGGGC 366

Db 279 ctgagagtgaacttcggcgccagccgcgcgccaccacacggaatctgcagagacagtgct 338
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Qy 367 CTCTTCTGTGACTTCGGCTCCCCGGCCAAACCGCAAGATCGGCTGTGCACCGC-CAAA-- 423

Db 339 gaggggagaccatgcgaatacaactccaaaatctaccagaaagcggaagcttcagccc 398
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Qy 424 GATGGTGTCCCTGCATCTTCGGTGTACGGTGTACCGCAGCGGAGATGCTCTTCACAGC 483

Db 399 aactgcaagcaccagtgtagtgcatagatggagctgtgggtgcatacccgctctgcceg 458
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Qy 484 AGTGCAACTACCACTGCCTGCCTGGACGGGGCGGTGGGTGCATGCCCCCTGTGCAGC 543

Db 459 caggagctctccctccccaaacctgggctgccccagccccaggtggtcaaaagtgcctggg 518
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Qy 544 ATGACGTTGCTGTGCCCCAGCCCTGACTGCCCTTCCCGAGGAGGGTCAAGCTGCCCGGG 603

Db 519 cagtgcgcgaggagtggtctgcgatgagagcaagga 556
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Qy 604 AATGCTGCGAGGAGTGGGTGTGTGACGAGGCCCAAGCA 641

RESULT 10
LOCUS MUSCYR61A 2018 bp mRNA ROD 12-JUN-1993
DEFINITION Mouse Cyr61 mRNA, complete cds.
ACCESSION M32490
KEYWORDS cyr61 product.
SOURCE Mouse (strain BALB/c) fibroblast cell line 3T3, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 2018)
AUTHORS O'Brien,T.P., Yang,G.P., Sanders,L. and Lau,L.F.
TITLE Expression of cyr61, a growth factor-inducible immediate-early gene
JOURNAL Mol. Cell. Biol. 10, 3569-3577 (1990)
MEDLINE 90287146
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by
L.F.Lau, 02-MAR-1990, for release after publication.

NCBI gi: 192909 Location/Qualifiers
source 1..2018
/organism="Mus musculus"
mRNA <1..2018
/note="Cyr61 mRNA"
CDS 190..1329
/note="Cyr61 product; NCBI gi: 309206"
/codon_start=1
/translation="MSSSTFRTLAVAVTLHLTRLALSTCPAACHCPLEAPKCAPGVG
LVRDGGCKVKAKQLNEDCSKTQPCDHTKGLCNFCASSTALKGICRAQSEGRPCEY
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WVCDEDSIKDSLDDQDDLGLDASEVELTRNNELIAIGKSSLIKRLPVFGTEPRVLFN
PLAHGQKCIIVQTTSWSQSKSCGTGISTRVTDNPECRLVKETRICEVRPCGPVYS
SLKKGKCSKTKKSPFVRETYAGCSSVKYRPKYCGSCVDGRCCPTLQTRTVKMRFR
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repeat_region 1453..1551
/note="49 bases repeat"
BASE COUNT 500 a 536 c 527 g 455 t
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DB 55; Score 88; Match 61.1%; QryMatch 4.2%; Pred. No. 1.39e-35;
Matches 243; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Db 865 aaatgcacgttcagaccacgtcttgggtccceagtgctccaagagctgcggaactggcacc 924
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Qy 721 AACTGCCTGGTCCAGACCACAGAGTGGAGCGGCTGTTCCAAGACCTGTGGGATGGGCATC 780

Db 925 tccacacgagttaccaatgacaacccagagtgccgcgctggtgaaagagagaccgggatctgt 984
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Qy 781 TCCACCCGGGTTACCAATGACAACGGCTCCTCGAGGCTAGAGAGCAGACGCCGCTGTGC 840

Db 985 gaagtgcgtccttgggacaaccagtgtagcagcagcctaaaaagggcaagaaatgcagc 1044
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Qy 841 ATGGTCAGGCCTTGGGAAGCTGACCTGGGAAGAGACATTAGAGAGGGCAAAAAGTGCATC 900

Db 1045 aagaccaagaatccccagaaaccagtcagattacttatgcaggatgtcccagtgccaag 1104
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Qy 901 CGTACTCCCAAAATCTCCAAGCCTATCAAGTTTGAGCTTCTGGCTGCACCAGCATGAAG 960

Db 1105 aaataccggcccaataactgcggctcctcgtagatggccggctgtgcacacctctgcag 1164
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Qy 961 ACATACCGAGCTAAATTCTGTGGAGTATGTACCGACGGCCGATGCTGCACCCCCACAGA 1020

Db 1165 accagaactgtgaagatgcggttcgcgatgcgaagatggagagatgtttcccaagaatgc 1224
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Qy 1021 ACCACCACCTGCCGTTGGAGTTCAAGTCCCTGACGGCGAGGTGATGAAGAAGACATG 1080

Db 1225 atgatgatccagtcctgcaaatgtaactacaactgcc 1262
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Qy 1081 ATGTTCATCAAGACCTGTGCTGCCATTACAACACTGTCC 1118

RESULT 11
LOCUS HSN0VH5 1469 bp DNA PRI 01-DEC-1994
DEFINITION H.sapiens novH gene exon 5.
ACCESSION X78354
KEYWORDS novH gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Elumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1469)
AUTHORS Martinerie,C., Huff,V., Joubert,I., Badzioch,M., Saunders,G.,
Strong,L. and Perbal,B.
TITLE Structural analysis of the human nov proto-oncogene and expression
in Wilms tumor
JOURNAL Oncogene 9 (9), 2729-2732 (1994)
MEDLINE 94336229
REFERENCE 2 (bases 1 to 1469)
AUTHORS Perbal,B.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-1994) to the EMBL/GenBank/DBJ databases. B.
Perbal, Institut Curie, Centre Universitaire Batiment 110, 91405
Orsay, Cedex, FRANCE
COMMENT NCBI gi: 587425
FEATURES Location/Qualifiers
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/tissue_type="placental"
/clone="IC110 clone 2"

REFERENCE 2 (bases 1 to 452)
AUTHORS Perbal,B.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-1994) to the EMBL/GenBank/DBBJ databases. B. Perbal, Institut Curie, Centre Universitaire Batiment 110, 91405 Orsay, Cedex, FRANCE
COMMENT NCBI gi: 587423

FEATURES
source Location/Qualifiers
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/chromosome="8"
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117..368
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BASE COUNT 111 a 96 c 117 g 128 t
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DB 46; Score 62; Match 65.0%; QryMatch 3.0%; Pred. No. 4.80e-19; Matches 134; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Db 121 agaggagataactgtgttctcgatgggtcatctaccgcagtgagagaaatttcagcc 180
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Qy 423 AGATGGTGTCCCTGCATCTTCGGTGGTACGGGTGTACCGCAGCGGAGAGTCCTTCCAGAG 482
Db 181 aagctgaaattccagtgcaactgcagagatgggcagattgctgtgtgcccgctgtca 240
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Qy 483 CAGCTGCAAGTACCAGTGCACGTGCTGGACGGGGCGGTGGATGCCCTTCCAGGGTCAAGCTGCCCGG 542
Db 241 gctggatgtgctactgcctgagcctaactgccagatcccaagaaagttaggtgcctgg 300
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Qy 543 CATGGACGTTGCTGTGCCCGACCCCTGACTGCCCTTCCGAGAGGGTCAAGCTGCCCGG 602
Db 301 agagtgtgtgaaagtggatctgtg 326
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Qy 603 GAAATGCTCGGAGGAGTGGGTGTGTG 628

RESULT 14
LOCUS MMCYR61G 5196 bp DNA ROD 20-MAY-1992
DEFINITION Mouse growth factor inducible immediate early gene cyr61.
ACCESSION X56790
KEYWORDS cyr61 gene; growth factor-inducible gene; immediate-early gene.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5196)
AUTHORS Lau,L.F.
TITLE Direct Submission

JOURNAL Submitted (14-NOV-1990) to the EMBL/GenBank/DBBJ databases. Lau L.F., University of Illinois College of Medicine, Dept. of Genetics (M/C 669), 808 South Wood Street, Chicago, IL 60611, USA
REFERENCE 2 (bases 1 to 5196)
AUTHORS Latinkic,B.V., O'Brien,T.P. and Lau,L.F.
TITLE Promoter function and structure of the growth factor-inducible immediate early gene cyr61
JOURNAL Nucleic Acids Res. 19 (12), 3261-3267 (1991)
MEDLINE 91288203
COMMENT Cry61 is an immediate early gene that is transcriptionally activated in T3T fibroblasts by serum, platelet-derived growth factor and the tumour protein TPA.
See M32490 for mRNA sequence.

NCBI gi: 50632
FEATURES
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WVCDEDSIKDSLDDQDDLGLDASEVELTRNNELIAIGKSSILKRLPVFGTEPRVLEN
PLAHGQKCIVQTTSWSQSKSCGTGISTRVNDNPECLRVKETRICEVRPCGQPVYS
SLKGGKCSKTKKSPVREFTYAGCSSVKYRPKYCGSCVDGRCCCTPLQTRTVKMRFR
CEDGEMFSKNVMMIQSCKNVCNCPHPNEASFRLYSLEFNDIHKFRD"
2315..2609
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2610..2823
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/number=2
2824..3167
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3168..3512
/gene="CYR61"
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3513..3633
/number=3
3634..3848
/gene="CYR61"
/number=4
3849..4078
/number=4
4079..>4381
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/number=5

polyA signal 5049..5054
BASE COUNT 1365 a 1355 c 1232 g 1244 t
ORIGIN

DB 53; Score 60; Match 67.0%; QryMatch 2.9%; Pred. No. 7.99e-18;


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Matches 118; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Db 3209 taccaaaacggggaagcttccagcccaactgtaaacaccagtgcaacatgtattgatggc 3268
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Qy 457 TACCGCAGCGGAGAGTCCCTCCAGAGCAGCTGCAATACCACTGCACGTGCCCTGGACGGG 516

Db 3269 gccgtggctgcattcctctgtgtccccagaactgtctctccccaatctggcgtgtccc 3328
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Qy 517 GCGGTGGGCTGCATGCCCTGTGCAGCATGGACGTTGGCTTGCCCCAGCCCTGACTGCCCC 576

Db 3329 aacccccggctggtgaagtcagcgggcagtgctgtgaagatgggtttgtgatga 3384
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Qy 577 TTCCCGAGGAGGTCAGCTGCCCGGCAATGCTGCGAGGAGTGGCTGTGTGACGA 632
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RESULT 15
LOCUS HSNVH12 557 bp DNA PRI 01-DEC-1994
DEFINITION H.sapiens novH gene exons 1 and 2.
ACCESSION X78351
KEYWORDS novH gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 557)
AUTHORS Martinerie,C., Huff,V., Joubert,I., Badziach,M., Saunders,G.,
Strong,L. and Perbal,B.
TITLE Structural analysis of the human nov proto-oncogene and expression
in Wilms tumor
JOURNAL Oncogene 9 (9), 2729-2732 (1994)
MEDLINE 94336229
REFERENCE 2 (bases 1 to 557)
AUTHORS Perbal,B.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-1994) to the EMBL/GenBank/DBJ databases. B.
Perbal, Institut Curie, Centre Universitaire Batiment 110, 91405
Orsay, Cedex, FRANCE
COMMENT NCBI gi: 587422
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X78354:159..455)
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VEVPGECEKWIICGDEEDSLGGLTLAAYRPEATLGEVSDSSVNCIEQTTEWTACSK
SCGMGFSTRVTNRNRQCEMLKQTRLCMVRPCEQEPEQPTDKKGKKCLRTKKSIAIHL
QFKNCTSLHTYKPRFCVSDGRCCTPHNTKTIQAEFQCSPQIVKRPMVMVIGTCTCH
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ORIGIN

DB 46; Score 52; Match 65.1%; QryMatch 2.5%; Pred. No. 4.80e-13;
Matches 112; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Db 343 cgcgcgcgacctgcgccccgggtgcgcgggtgtgtggacggctgctcatgtgtctgg 402
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Qy 245 CGGCGCGCGGCTGCCCGGGCGGCTGAGCCTCGTGTGGACGGCTGGGCTGCTGCCGCG 304

Db 403 tgtgtgccgccagcgtgcgcgagagctgtcagatctggagccatggcagcagagcagtg 462
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Qy 305 TCTGCGCCAAGCAGCTGGCGGAGCTGTGCACCGAGCGGACCCCTGCGACCCGACACAGG 364

Db 463 gcctctactgtgatcgcagcgcgggaccccaagcaaccagactggcatctgcac 514
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Qy 365 GCCTCTTCTGTACTTCGGCTCCCGCGCCCAACCGCAAGATCGGCGTGTGCAC 416

Search completed: Fri Sep 22 22:17:14 1995
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22 62 3.0 429 19 R16276 ya48d02.r1 Homo sapie 1.18e-56
c 23 62 3.0 377 57 T92863 ye27f01.r1 Homo sapie 1.18e-56
c 24 53 2.6 58 55 T86143 y84f01.s1 Homo sapie 1.41e-42
25 38 1.8 93 17 R09732 yf27a12.s1 Homo sapie 9.86e-21
26 37 1.8 438 26 R43932 yg22d07.s1 Homo sapie 2.23e-19
27 37 1.8 437 29 R54590 yg81h09.s1 Homo sapie 2.23e-19
c 28 37 1.8 399 45 T47099 yb52c08.s1 Homo sapie 2.23e-19
29 37 1.8 273 35 T07122 EST05011 Homo sapiens 2.23e-19
c 30 37 1.8 37 16 R06912 yf12g05.s1 Homo sapie 2.23e-19
c 31 36 1.7 525 51 T71627 yd36f08.s1 Homo sapie 4.87e-18
32 36 1.7 356 53 T80892 yd26h11.r1 Homo sapie 4.87e-18
33 35 1.7 265 47 T58750 yb80e05.s1 Homo sapie 1.02e-16
c 34 34 1.6 285 58 T96616 ye51e04.s1 Homo sapie 2.05e-15
35 34 1.6 485 56 T89955 ye13b10.r1 Homo sapie 2.05e-15
36 33 1.6 169 6 HSC05A082 H. sapiens partial cD 3.94e-14
37 33 1.6 169 10 HSC2TC062 H. sapiens partial cD 3.94e-14
c 38 33 1.6 387 56 T91101 yd51c05.s1 Homo sapie 3.94e-14
39 32 1.5 331 35 T07131 EST05020 Homo sapiens 7.22e-13
c 40 32 1.5 475 32 R63483 y108f10.r1 Homo sapie 7.22e-13
41 32 1.5 460 58 T97712 ye54e02.s1 Homo sapie 7.22e-13
42 32 1.5 358 47 T57458 yb51h09.r1 Homo sapie 7.22e-13
43 32 1.5 251 28 R50724 yj58d01.s1 Homo sapie 7.22e-13
44 32 1.5 327 4 HSA0AAVGP H. sapiens putatively 7.22e-13
c 45 32 1.5 427 29 R51961 yj71h01.r1 Homo sapie 7.22e-13
```

ALIGNMENTS

```
RESULT 1
LOCUS T98687 506 bp mRNA EST 31-MAR-1995
DEFINITION ye61b01.r1 Homo sapiens cDNA clone 122185 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);
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ACCESSION T98687
KEYWORDS EST.
SOURCE human clone=122185 library=Soares fetal liver spleen lNfLS
vector=pT7r3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13Rp1 Rsite1=Pac I Reite2=Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGCAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
```

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 506)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfling,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 303

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 748424

FEATURES
source Location/Qualifiers
1..506
/organism="Homo sapiens"
/clone="122185"
/note="human"
BASE COUNT 131 a 114 c 130 g 124 t 7 others
ORIGIN

DB 58; Score 291; Match 96.3%; QryMatch 14.0%; Pred. No. 0.00e+00;
Matches 315; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

Db 1 acaacgcctcctgcaggctagagaagcaganc-gcctgtcatggtcaggccttgcgaaac 59
|||||
Qy 800 ACAACGCCCTCCTGCAGGCTAGAGAAGCAGACGCCGCTGTGCATGGTCAGGGCCTTGGGAAG 859

Db 60 ngancctggaagagaacattaagaaggggcaaaaagtgcacgtactctcccaaatctcca 119
|||||
Qy 860 CTGACCTGGAAGAGAACATTAAGAAGGGCAAAAGTCGATCCGTACTCCCAAAATCTCCA 919

Db 120 agcctatacaagtttgagctttctggtgcaccagcatgaagacataccgagctaaattct 179
|||||
Qy 920 AGCCTATCAAGTTTGAGCTTTCTGGCTGCACCAGCATGAAGACATACCGAGCTAAATTCT 979

Db 180 gtggagtgatgtaccgacggccgcatgtgcacccccacagacacccacctgccggtgg 239
|||||
Qy 980 GTGAGTATGTACCGACGGCCGATGCTGCACCCCCACAGAACCCACCCCTGCCGGTGG 1039

Db 240 agttcaagtgcctgacgcgaggtcatgaagaagaacatgatgttcattcaagacctgt 299
|||||
Qy 1040 AGTTCAAGTGCCTGCACGGCGAGGTGATGAAGAAGACATGATGTTTCAT-CAAGACCTGT 1098

Db 300 gcctgccatttaacaactgttccccgga 326
|||||
Qy 1099 GCCTGCCATT-ACAACTGTCCCGGAGA 1124

RESULT 2
LOCUS T92313 264 bp mRNA EST 22-MAR-1995
DEFINITION ye18g08.r1 Homo sapiens cDNA clone 118142 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);

ACCESSION T92313
KEYWORDS EST.
SOURCE human clone=118142 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13Rp1 Rsite1=EcoRI Reite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCGAGTTT-TTTT-TTTT-TTTT-TTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 264)

REFERENCE Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
AUTHORS Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfling,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 249
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 724226
FEATURES
source

BASE COUNT 73 a 71 c 63 g 56 t 1 others
ORIGIN

DB 56; Score 249; Match 98.9%; QryMatch 12.0%; Pred. No. 0.00e+00;
Matches 261; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Db 1 aaatctcaagcctatcaagtttgagctttctggctgcaccagcatgaagacataccgag 60
|||||
Qy 911 AATCTCCAAGCCTATCAAGTTTGAGCTTTCTGGCTGCACCAGCATGAAGACATACCGAG 970
Db 61 ctaaatctgtgagtatgtaccgacggcgcatgtgtcacccccacagaacaccacc 120
|||||
Qy 971 CTAATTTCTGTGGAGTATGTACCGACGGCCGATGCTGCACCCCCACAGAACCACCC 1030
Db 121 tgcggtngagttcaagtgccctgacggcgaggtcatgaagaagaacatgatgttcata 180
|||||
Qy 1031 TGCCGGTGCAGTTCAAGTGCCTGACGGCGAGGTCTATGAAGAAGACATGATGTTTCATCA 1090
Db 181 agacctgtcctgcctacattacaactgtcccgagagacaatgacatctttggaaatcgctgtac 240
|||||
Qy 1091 AGACCTGTGCCTGCCATTACAACCTGTCCGCGAGACATGACATCTTTG-AATCGCTGTAC 1149
Db 241 tacaggaagatgtacggagacat 264
|||||
Qy 1150 TACAGG-AAGATGTACGGAGACAT 1172

RESULT 3
LOCUS T86251 434 bp mRNA EST 17-MAR-1995
DEFINITION yd84f01.r1 Homo sapiens cDNA clone 114937 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);
ACCESSION T86251
KEYWORDS EST.
SOURCE human clone=114937 library=Soares fetal liver spleen INFLS
vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13RP1 Reitel=Pac I Reite2=Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGGAGAATTAATAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pf7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 434)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 301
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 714603
FEATURES
source

BASE COUNT 117 a 81 c 111 g 119 t 6 others
ORIGIN

DB 55; Score 245; Match 94.7%; QryMatch 11.8%; Pred. No. 0.00e+00;
Matches 302; Conservative 0; Mismatches 9; Indels 8; Gaps 6;

Db 2 aatagtctatcaacccagacactggttgaagaatgtaagacttgacagtggaaactac 61
|||||
Qy 1343 AATAGTCTATCTTCCCCAGACACTGGTTTGAAGAATGTTAAGACTTGACAGTGGAACTAC 1402

Db 62 attagtacacagcaccagaatgtatatattaagtggtgcttttagagagcagtgggagggtac 121
|||||

Qy 1403 ATTAGTACACAGCACCAAGAATGTATATTAAAGCTGGCTTTAGGAGCAGTGGAGGGGTAC 1462

Db 122 cagcagaaaggtttagtatcatcagatagcatcttatcacgagtaatatgcctgctatttga 181
|||

Qy 1463 CGGCCC---GGTTACTATCATCAGATCGGACTCTTATACGAGTAATATGCCCTGCTATTGGA 1519

Db 182 agtgaattgagaagaaaatttttagcgtgctcaactgacctgacctgtagcctcagtgaca 241
|||||

Qy 1520 AGTGTAATTGAGAAGGAAAAATTTTAGCGTGTCTCACTGACCTGCCTGTAGCCCCAGTGACA 1579

Db 242 gctaggatgtggcattctccagcccatccaaggagactgagtcgaagttgttcnttaagtc 301
|||||

Qy 1580 GCTAGGATGTG-CATTCTCCAGCCATC-AAG-AGACTGAGTCAAGTTGTTCC-TTAAGTC 1635

Db 302 aggaacagcagactcagct 320
||

Qy 1636 AG-AACAGCAGACTCAGCT 1653

RESULT 4
LOCUS R37906 345 bp mRNA EST 04-MAY-1995
DEFINITION yh97e04.r1 Homo sapiens cDNA clone 137694 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);
ACCESSION R37906

KEYWORDS EST.
SOURCE human clone=137694 library=Soares placenta Nb2HP vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RPI Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGGAAGAATTGCGGCGCAGCAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 345)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 262
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 795362 Location/Qualifiers
source 1..345
/organism="Homo sapiens"
/clone="137694"
/note="human"
BASE COUNT 108 a 62 c 83 g 90 t 2 others
ORIGIN
DB 25; Score 236; Match 95.2%; QryMatch 11.4%; Pred. No. 0.00e+00;
Matches 279; Conservative 0; Mismatches 8; Indels 6; Gaps 6;
Db 1 caggaagatgtacgcagacatggcatgaagccagagagtgcagacattaactcattaga 60
|||||
Qy 1152 CAGGAAGATGTACGGAGACATGGCATGAAGCCAGAGATGAGACACATTAACTCATTAGA 1211
Db 61 ctggaacttgaactgattcacatctcattttccgtaaaaatgatttcagtagcacacaagt 120
|||||
Qy 1212 CTGGAACCTGAACTGATTCACATCTCATTTTTCCGTAAAAATGATTTTCAGTAGCACACAAGT 1271
Db 121 tatttaaatctgttttctaactgggggaaagattccccaccattccaaacattcgaactgtgc 180
|||||
Qy 1272 TATTTAATCTGTTTTCTAACTGGGGGAAAGATTTCCCAACCAATTCAAAACATTGTGC 1331
Db 181 catgtcaacaacaatagtctatncaaccccgacacactgggttgaaggaaatggttaagacttg 240
|||||
Qy 1332 CATGTCAACAATAAGTCTAT-CTTCCCCACACACTGGTTTGAAG-AATGTTAAGACTTG 1389
Db 241 acagtgggaactacattagttacacagccaccagggaatgtnthtttaagggtg 293

QY 1390 ACAGTGG-AACTACATTAGT-ACACAG-CACCAG-AATGTATATTAAAGGTGTG 1438
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
RESULT 5 T98574 420 bp mRNA EST 31-MAR-1995
LOCUS ye60a12.r1 Homo sapiens cDNA clone 122110 5' similar to gb:M92934
DEFINITION CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);
ACCESSION T98574
KEYWORDS EST.
SOURCE human clone=122110 library=Soares fetal liver spleen 1NFLS
vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13RPI Rsite1=Pac I Rsite2=Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGGAAGAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 420)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 232
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 748311 Location/Qualifiers
source 1..420
/organism="Homo sapiens"
/clone="122110"
/note="human"
BASE COUNT 106 a 99 c 111 g 96 t 8 others
ORIGIN
DB 58; Score 209; Match 95.6%; QryMatch 10.1%; Pred. No. 2.67e-317;
Matches 259; Conservative 0; Mismatches 4; Indels 8; Gaps 7;
Db 12 gacaacgcctcctgcaggtagagaagcaganc-gcctgtgcattggtcaggccttgcca- 69
|||||
Qy 799 GACAACGCCTCCTCGAGGCTAGAGAGACAGCCGCTGTGCATGGTCAGGCCTTGGGAA 858
Db 70 -cngacctggaagaacattagaagggcaaaaagtcactcgtactcccaaatcc 128
|
Qy 859 GCTGACCTGGAAGAGAACATTAGNAGGGGCAAAAGTCATCCGTACTCCCCAAATCTCC 918

Db 129 aagcctatcaagtttgagctttctggtgcaccagatgaagacataccgagctaaattc 188
|||||
Qy 919 AAGCCTATCAAGTTTGAGCTTCTGGCTGCACCAGCATGAACACATACCGAGCTAAATTC 978

Db 189 tqtgggagtatgtaccgaagccgctgctgcaccccttacagaaccaccacccctgcgg 248
|||||
Qy 979 TGTGG-ACTATGTACCGACGGCCGATGCTGCACCCCCC-ACAGAACACCACCCCTGCCGG 1036

Db 249 tggagtttcaagttgcccttgacggcgaggt 279
|||||
Qy 1037 TGGAGTT-CAAGT-GCCCT-GACGGCGAGGT 1064

RESULT 6
LOCUS R06961 376 bp mRNA EST 05-APR-1995
DEFINITION yf12g05.r1 Homo sapiens cDNA clone 126680 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);

ACCESSION R06961
KEYWORDS EST.
SOURCE human clone=126680 library=Soares fetal liver spleen INFLS
vector=pT73D (Pharmacia) with a modified polylinker host=DHI08
(ampicillin resistant) primer=M13RP1 Reitel=Pac I Reite2=Eco RI
Liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5'
AACTGGAAGCAATTAATTAAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 376)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 235
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 758884
FEATURES source
Location/Qualifiers
1..376
/organism="Homo sapiens"
/clone="126680"
/note="human"

BASE COUNT 95 a 93 c 98 g 87 t 3 others
ORIGIN

DB 16; Score 206; Match 96.3%; QryMatch 9.9%; Pred. No. 9.94e-312;
Matches 235; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

Db 1 acaagcctcctgcaggctagagaagcagagccgctgtgcatggtcaggccttgcggaag 60
|||||
Qy 800 ACAACGCCTCCTGCAGGCTAGAGAAGCAGAGCCGCCTGTGCATGGTCAGGCCCTTGCGAAG 859

Db 61 tgaacctggaagagaacattaaagagggaacaaagtgcacgtactccccaaattcca 120
|||||
Qy 860 CTGACCTGGAAGAGAACATTAAGAAGGGCAAAAGTGCATCGTACTCCCAAAATCTCCA 919

Db 121 agcctataagtttgagctttctggtgcaccagcatgaagacataccgagctaaattc 180
|||||
Qy 920 AGCCTATCAAGTTTTCAGCTTCTGCTGCACGAGCATGAAG-ACATACCGAGCTAAATTC 978

Db 181 tgtgggagtatgtaccgacggccgctgctgcaccccttacaggaaccaccacccctgcg 240
|||||
Qy 979 TGTGG-ACTATGTACCGACGGCCGATGCTGCACCCCCC-ACAG-AACCACACCCCTGCCG 1035

Db 241 gtgg 244
|||||
Qy 1036 GTGG 1039

RESULT 7
LOCUS T49714 357 bp mRNA EST 08-FEB-1995
DEFINITION ya80a10.r1 Homo sapiens cDNA clone 67962 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN).

ACCESSION T49714
KEYWORDS EST.
SOURCE human clone=67962 library=Stratagene ovary (#937217)
vector=Bluescript SK host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Cloned unidirectionally.
Primer: Oligo dT. Total ovary tissue, normal 49 year old caucasian
female. Average insert size: 0.8 kb; Uni-ZAP XR Vector; 5' adaptor
sequence: 5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 357)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Other ESTs: ya80a10.s1
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 254
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 651574
FEATURES Location/Qualifiers
1..357
/organism="Homo sapiens"
/clone="67962"
/note="human"

BASE COUNT 96 a 54 c 83 g 124 t
ORIGIN

DB 45; Score 198; Match 99.5%; QryMatch 9.5%; Pred. No. 6.14e-297;
Matches 204; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 taatgcttgatattcaatgttagcctcaatttctgaacaccataggtagaatgtaaaag 60
|||||
Qy 1867 TAATGCTTTGATATTTCAATGTTAGCCTCAATTTCTGAACACCATAGCTAGATAAG 1926
|||||

Db 61 cttgtctgatcgttcaaagcatgaaatggatacttatatggaattctgctcagatagaa 120
|||||
Qy 1927 CTTGCTCTGATCGTTCAAAGCATGAAATGGATACCTTATATGGAATTTCTGCTCAGATAGAA 1986
|||||

Db 121 tgacagtcctgcaaaacagattgttgcaaggaggcagtcagtgtccttggcaggctg 180
|||||
Qy 1987 TGACAGTCCTCAAAACAGATTTGTTGCAAAGGGGAGGCATCAGTGTC-TTGGCAGGCTG 2045
|||||

Db 181 atttctaggtaggaaatgtggtagc 205
|||||
Qy 2046 ATTTCTAGGTAGGAAATGTGGTAGC 2070
|||||

RESULT 8
LOCUS T92598 331 bp mRNA EST 22-MAR-1995
DEFINITION ye26f01.s1 Homo sapiens cDNA clone 118873 3' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);.
ACCESSION T92598
KEYWORDS EST.
SOURCE human clone=118873 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=-21ml3 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 331)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 172
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 724511
Location/Qualifiers
1..331
/organism="Homo sapiens"
/clone="118873"

FEATURES
source

BASE COUNT 89 a 53 c 73 g 113 t 3 others
ORIGIN

DB 56; Score 187; Match 99.5%; QryMatch 9.0%; Pred. No. 1.16e-276;
Matches 193; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 2 tatttcaatgttagcctcaatttctgaacaccataggtagaatgtaaagcttgtctgatc 61
|||||
Qy 1878 TATTTCAATGTTAGCCTCAATTTCTGAACACCATAGGTAGAATGTAAAGCTTGTCTGATC 1937
|||||

Db 62 gttcaaaagcatgaaatggatacttatatggaattctgctcagatagaaatgacagtcctg 121
|||||
Qy 1938 GTTCAAAGCATGAAATGGATACCTTATATGGAATTTCTGCTCAGATAGAAATGACAGTCCGT 1997
|||||

Db 122 caaaacagattgttgcaaggaggcagtcagtgtccttggcaggctgatttctaggt 181
|||||
Qy 1998 CAAAACAGATTGTTTGCAAAGGGGAGGCATCAGTGTC-TTGGCAGGCTGATTTCTAGGTA 2056
|||||

Db 182 ggaatgtggtagc 195
|||||
Qy 2057 GGAATGTGGTAGC 2070
|||||

RESULT 9
LOCUS T65929 410 bp mRNA EST 20-FEB-1995
DEFINITION yc24e08.s1 Homo sapiens cDNA clone 81638 3' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);.
ACCESSION T65929
KEYWORDS EST.
SOURCE human clone=81638 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=-21ml3 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 410)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 377
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674974
Location/Qualifiers
1..410
/organism="Homo sapiens"

FEATURES
source

```

/clone="81638"
/note="human"

BASE COUNT      143 a      82 c      68 g      114 t      3 others
ORIGIN

DB 49; Score      172; Match 96.7%; QryMatch 8.3%; Pred. No. 3.81e-249;
Matches 208; Conservative 0; Mismatches 1; Indels 6; Gaps 6;

Db 196 gctaccacatttcctacctaagaatcagcctgccaagacactgatgcctccctttgca 255
|||||
Cp 2070 GCTACCAcATTTCCTACCTAGAAATCAGCCTGCCAAG-ACACTGATGCTCCCTTTGCA 2012
|||||

Db 256 aacaatctgtttgacggactgtcattctatctgagcagaattccatataagtatccat 315
|||||
Cp 2011 AACAACTGTTTTGACGGACTGTCTATTCTATCTGAGCAGAAATTCCATATAAGTATCCAT 1952
|||||

Db 316 ttcattgctttgaacgatcagacaagctttacattctacattgngnggttcaggaaattga 375
|||||
Cp 1951 TTCATGCTTTGAACGATCAGACAAGCTTTACATTCTACCTATGGTG-TTCAG-AAATTGA 1894
|||||

Db 376 gggctaacattggaaatatcaaaaggcattaaaaac 410
||
Cp 1893 GG-CTAACATTG-AAATATCAAAG-CATTAAAAAC 1862
|||||
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RESULT 10
LOCUS      T49715      408 bp      mRNA      EST      08-FEB-1995
DEFINITION ya80a10.s1 Homo sapiens cDNA clone 67962 3' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN).
ACCESSION  T49715
KEYWORDS   EST.
SOURCE     human clone=67962 library=Stratagene ovary (#937217)
vector=Bluescript SK host=SOLR cells (kanamycin resistant)
primer=-21m13 Rsite1=EcoRI Rsite2=XhoI Cloned unidirectionally.
Primer: Oligo dT. Total ovary tissue, normal 49 year old caucasian
female. Average insert size: 0.8 kb; Uni-ZAP XR Vector; 5' adaptor
sequence: 5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTT-3'.
```

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ORGANISM  Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 408)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE     WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Other ESTs: ya80a10.r1
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 364
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
```

```

NCBI gi: 651575
Location/Qualifiers
source      1..408
```

```

/organism="Homo sapiens"
/clone="67962"
/note="human"

BASE COUNT      133 a      82 c      65 g      118 t      10 others
ORIGIN

DB 45; Score      169; Match 94.0%; QryMatch 8.1%; Pred. No. 1.16e-243;
Matches 189; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

Db 204 gctaccacatttcctacctaagaatcagcctgccaagacactgatgcctccctttgca 263
|||||
Cp 2070 GCTACCAcATTTCCTACCTAGAAATCAGCCTGCCAAG-ACACTGATGCTCCCTTTGCA 2012
|||||

Db 264 aacaatctgtttgacggactgtcattctatctgtngcagantttccatatatngnatccat 323
|||||
Cp 2011 AACAACTGTTTTGACGGACTGTCTATTCTATCTGAGCAGAAATTCCATATAAGTATCCAT 1952
|||||

Db 324 ttcattgctttgaacntcagncagctttacattctacattgggttcagnaattgag 383
|||||
Cp 1951 TTCATGCTTTGAACGATCAGACAAGCTTTACATTCTACCTATGCTGTTTCAG-AAATTGAG 1893
|||||

Db 384 gctaacattggaaatatccaa 404
|||||
Cp 1892 GCTAACATTG-AAATATCAAA 1873
|||||
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RESULT 11
LOCUS      T53387      365 bp      mRNA      EST      08-FEB-1995
DEFINITION ya88f03.r1 Homo sapiens cDNA clone 68765 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN).
ACCESSION  T53387
KEYWORDS   EST.
SOURCE     human clone=68765 library=Stratagene placenta (#937225)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Placental tissue from a
Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTT-3'.
```

```

ORGANISM  Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 365)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE     WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Other ESTs: ya88f03.s1
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 311
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
```

```

NCBI gi: 655247
Location/Qualifiers
```

source 1..365
/organism="Homo sapiens"
/clone="68765"
/note="human"
BASE COUNT 108 a 54 c 78 g 125 t
ORIGIN
DB 46; Score 167; Match 99.4%; QryMatch 8.0%; Pred. No. 5.21e-240;
Matches 173; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 4 ttctgaacaccataggtagaatgtaaaagcttgctgctgattcgttcacaaagcatgaaatggat 63
|||||
QY 1998 TTCTCGAACACCATTAGGTAGATGTAAAGCTTGCTGATCGTTCAAAAGCATGAAATGGAT 1957
Db 64 acttatatggaattctgctcagatagaatgacagtcogtcacaaacagattgtttgcaaa 123
|||||
QY 1958 ACTTATATGGAATTTCTGCTCAGATAGAAATGCAGTCGCTCGTCAAAACACAGATTGTTGCCAAA 2017
Db 124 ggggaggeatcagtgccttggcaggctgatttcttaggtaggaaatgtggtagc 177
|||||
QY 2018 GGGAGGCATCAGTGTCTTGGCAGGCTGATTTCTAGTAGGAAATGTGGTAGC 2070

RESULT 12
LOCUS T53524 205 bp mRNA EST 08-FEB-1995
DEFINITION ya96b01.r1 Homo sapiens cDNA clone 69481 5' similar to gb:M92934
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN).
ACCESSION T53524
KEYWORDS EST.
SOURCE human clone=69481 library=Stratagene placenta (#937225)
vector=pBluescript SK- host=S01R cells (kanamycin resistant)
primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Placental tissue from a
Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCAGTGTTTT-TTTT-TTTT-TTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 205)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

NCBI gi: 655384
Location/Qualifiers
source 1..205

/organism="Homo sapiens"
/clone="69481"
/note="human"
BASE COUNT 29 a 43 c 42 g 51 t 40 others
ORIGIN
DB 46; Score 157; Match 78.8%; QryMatch 7.6%; Pred. No. 8.41e-222;
Matches 160; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Db 3 tatgctnctntttgngtgtnattaaagangannatttngcncnctcactgacctgcc 62
|||||
QY 1504 TATGCCTGCTATTTGAAAGTGTAAATTGAGAAGGAAAAATTTAGCGTCTGCTGACTGACCTGCC 1563
Db 63 tntagcccccngtgacngctngganntgcattctnccnccntcnnagagactgagtcnagtt 122
|||||
QY 1564 TGTAGCCCCAGTGACAGCTAGGATGTGCATTCTCCAGCCATCAAGAGACTGAGTCAAGTT 1623
Db 123 gttccttnagncngaacngcngactcngcncctgcacttctgnttcgntgtacacngttca 182
|||||
QY 1624 GTTCCTTAAGTCAGAACAGCAGACTCAGCTCTGACATTTCTGATTCCAATGCACACTGTTCA 1683
Db 183 gggnnccgggacacctgcgattag 205
|||
QY 1684 GGAATCGGAATCCTGTCGATTAG 1706

RESULT 13
LOCUS T27642 404 bp mRNA EST 04-JAN-1995
DEFINITION EST10485 Homo sapiens cDNA 3' end similar to connective tissue
growth factor (HT:1399).
ACCESSION T27642
KEYWORDS EST.
SOURCE human library=Human Adipose tissue primer=M13-21.
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 404)
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL Unpublished (1995)
COMMENT Other_ESTs: EST10484 THC23588
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

FEATURES source NCBI gi: 609740 Location/Qualifiers 1..404 /organism="Homo sapiens" /note="human" BASE COUNT 140 a 82 c 67 g 113 t 2 others ORIGIN

DB 39; Score 155; Match 95.3%; QryMatch 7.5%; Pred. No. 3.59e-218; Matches 204; Conservative 0; Mismatches 2; Indels 8; Gaps 8;

Db 191 gtaccacatttctacctaagaatcagcctgccaaggacactgatgcctccctttgca 250 ||||| GCTACCACATTTCCTACCTAGAAATCAGCCTCGCCAAG-ACACTGATGCCCTCCCTTTGCA 2012

Db 251 aacaatctgttttgacgggactgtcattctatctgacaggaatttccatataagtatcc 310 ||||| AACAAATCTGTTTTCACGG-ACTGTCATTCTATCTGAGCAG-AATTTCATATAAGTATCC 1954

Db 311 atttcattgttgacgggtcagacaaagctttacattctacctatgngggttcagaaaattg 370 ||||| ATTTTCATGCTTTTGACGATCAGACAAGCTTTACATTCTACCTATGCTG-TTCAGAAAATTG 1895

Db 371 agggctaaccattgaaaatatcaaggcattaaa 404 ||||| AGG-CTAAC-ATTG-AAATATCAAG-CATTAAA 1865

RESULT 14 LOCUS T64503 140 bp mRNA EST 20-FEB-1995 DEFINITION yc24e08.r1 Homo sapiens cDNA clone 81638 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);. ACCESSION T64503 KEYWORDS EST. SOURCE human clones-81638 library=Stratagene lung (#937210) vector=pBluescript SK- host=SOLR cells (kanamycin resistant) primer=M13RP1 Reitel=EcoRI Reite2=XhoI Normal lung tissue from a 72 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 140) AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R. WASHU-Merck EST Project Unpublished (1995)

Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES source NCBI gi: 673548 Location/Qualifiers 1..140 /organism="Homo sapiens" /clone="81638" /note="human" BASE COUNT 39 a 39 c 36 g 25 t 1 others ORIGIN

DB 49; Score 139; Match 99.3%; QryMatch 6.7%; Pred. No. 2.86e-189; Matches 139; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 tgaagacataccgagctaaattctgtggagtgtaccgacggnctgctgcaccccc 60 ||||| TGAAGACATACCGAGCTAAATCTCTGGAGTATGTACCGACGGCCGATGCTGCACCCCC 1015

Db 61 acagaaccacacccctgccgtggagttcaagtccctgacgggaggtcatgaagaaga 120 ||||| ACAGAACCAACCCCTGCCGTGGAGTTCAAGTCCCTGACGGCGAGTCAAGAAGA 1075

Db 121 acatgatgttcataagacc 140 ||||| ACATGATGTTTCATCAAGACC 1095

RESULT 15 LOCUS HHEA46W 326 bp RNA EST 18-AUG-1994 DEFINITION H. sapiens partial cDNA sequence; clone HEA46W; single read. ACCESSION Z36725 KEYWORDS partial cDNA sequence; transcribed sequence fragment. SOURCE human. ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 326) AUTHORS Genexpress. TITLE Direct Submission JOURNAL Submitted (12-AUG-1994) to the EMBL/GenBank/DBJ databases. Genzentrum Muenchen, Laboratorium fuer molekulare Biologie, Am Klopferspitz 18a, 82152 Martinsried, Germany. E-mail: obermaier@vms.biochem.mpg.de

REFERENCE 2 (bases 1 to 326) AUTHORS Genexpress. TITLE The Genexpress cDNA program JOURNAL Unpublished COMMENT cloning vector is pBluescript SK(+); Genexpress library reference is A. automatic.

FEATURES source NCBI gi: 531575 Location/Qualifiers 1..326 /organism="Homo sapiens" /clone_lib="Atrium cDNA library Human heart" BASE COUNT 113 a 68 c 48 g 97 t ORIGIN

DB 3; Score 124; Match 99.2%; QryMatch 6.0%; Pred. No. 1.88e-162;

	Matches	130;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
Db	196	gctaccacatttctactacctagaaatcagcctgccaggacactgatgcctcccttttgca								255
Cp	2070	GCTACGACATTTCCTACCTAGAAATCAGCCTGCCAAG-ACACTGATGCCTCCCTTTTCCA								2012
Db	256	aacaatctgttttgacggactgtcattctatctgagcagaatttccatataagtatccat								315
Cp	2011	AACAACTCTTTTGACGGACTGTCTATCTGAGCAGAAATTCGATATAAGTATCCAT								1952
Db	316	ttcatgctttg								326
Cp	1951	TTCATGCTTTG								1941

Search completed: Fri Sep 22 21:57:17 1995
Job time : 425 secs.